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AI392674 tg47c02.x
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9D_est25:*
9D_est23:*

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gb_gss13:*
gb_gss14:*
gb_gss14:*
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1001:
1002:
1004:
  Result Sco
                                                                                                                                       April 5, 2000, 18:38:42; Search time 6423.57 Seconds (Without alignments) 2513.359 Million cell updates/sec
                                                                                                                                                                                                                       US-09-090-672B-1
4276
1 TICIACCGITITITCCCTGC......ATCAGAAAAAAAAAAAA 4276
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9077268
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          4538634 seqs, 1887831982 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                            OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Sequence:
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High quality sequence stop: 444. Location/qualifiers 1. 506 1. 506	Ouery Match Ouery Match 9.0%; Score 386; DB 45; Length 506; Best Local Similarity 99.8%; Pred. No. 1.2e-136; Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1; QY 3762 ACATATGAACTCCTTTTCGTATTGCCATCGGGTTCCATGGAGTTTATTCTTTGTT 3821		4182 GACCAGCATTATAATTTCAGGGTTTTGAGGCTCAACATAATTTCATTATCCTCA 4
H71225 ys12e09.r1 H71226 ys12e09.s1 AA77228 Z19960 HSAAABDCI B AA381126 EST94221 AA634469 zu76a06.s AA1802170 tx25b02.x AA782211 ai47h12.s AA903370 ox88c02.s AA917896 zv05e07.s T93967 yd56d10.s1 AA03888 aga30d05.s AA381125 EST94220 H77530 yr05b10.r1 AQ883641 HS_5478_B T15585 yd56d10.r1 AQ883641 HS_5478_B T15585 yd56d10.r1 AQ883641 HS_55010.s1 AA38125 EST94220 H775436 wg57a05.x B5578 CIT-HSP-2 AA350648 EST58017 AA350648 EST58017 AA350648 EST58017		EST sapiens CDN	raniata; Vertebrata; Mammalia; Hominidae; Homo. h.gov/ncicgap. er Genome Anatomy Project (CGAP), ersion replaced gi:2151612. b. v. 'free through LLNL; contact the nl.gov) for further information.
328 8.1 398 24 H71225 329 7.5 529 38 AAB11226 302 7.5 529 32 AAB11226 302 7.1 302 33 AAB11226 244 5.7 364 36 AAB11226 193 4.5 274 38 AAB1221 194 4.5 221 39 AAB2211 187 4.4 385 21 793967 186 4.3 365 42 AAB2231 156 3.6 42 385 31 AAB1125 115 3.6 42 385 31 AAB1125 113 3.2 559 88 AAB3304 113 3.2 559 81 AAB3304 113 269 81 B55278 46 1.1 269 32 AAB50648 46 1.1 269 32 AAB50648	1.1 4.26 1.00 1	A 1392674 50.6 bp 1392674 1392674 1392674 1392674 1392674 13966 23 13969 2673 13969 2673 17996 3', mRN	
000 0 000000 0 000 0 000 000 000 000 0		C 41 42 44 44 45 45 FESULT 1 A1392674/C LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

3

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H71226 438 bp mRNA EST 26-OCT-1995
ys12e09.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:214600 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia:
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 438)
Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Locy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mag, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags
Genome_Res. 6 (9), 807-828 (1996)
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Insert Slze: 1184
High quality sequence stops: 372
Source: INAGE Consortium, LLNI
This clone is avallable royalty free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1184 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stops: 372.
Location/Qualifiers
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97044478
On Sep 21, 1992 this sequence version replaced gi:276076. Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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/db_xref="GDB:3779904"
/db_xref="taxon:9606"
/clone="IMAGE:214600"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 329; DB 24; Length 438; 100.0%; Pred. No. 5.7e-115; tive 0; Mismatches 0; Indels
                                                                                                                                                                 489 AAACTATATTTGTTGGTGGTGTTCCTCGACCATTACGAGCTGTGGAGC 536
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H71226.1 GI:1043042
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Best Local Similarity 100.
Matches 329; Conservative
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AUTHORS
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//dev_stage="20 week-post conception fetus"
//deb.host="DH10B (ampicillin resistent)"
//deb.host="DH10B (ampicillin resistent)"
//deb.host="DH10B (ampicillin resistent)"
//deb.host="Contain the pact of the primer of strand contain the pact of the primer of the pact of the primer of the pact of the pact of the pact of the modified primer of the m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Sep 21, 1992 this sequence version replaced gi:276075.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1184
High quality sequence stops: 387
Source: IMAGE Consortium, LLNL
This clone is avaliable royalty-free through LLNL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Insert Length: 1184 Std Error: 0.00
Seq primar: Mishel
High quality sequence stop: 387.
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                                                             Homo sapiens

Bukaryota: Merazoa: Chordata; Craniata; Vertebrata; Mammalia;

Butheria: Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 398)

1 (bases 1 to 398)

1 (bases 2 to 398)

1 (bases 3 to 398)

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.

Mardis, E., Moore, B., Morris, M., Parsons, J., Pranqe, C., Rifkin, L.,

Rohling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.

Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:214600"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 398;
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100.0%; Pred. No. 3.6e-122;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 348; Conservative
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T-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacta), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacta). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 329
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homon Liver tissue"
// Clone_lib="B, Human Liver tissue"
// note="Yector: gtl1: clone_library=B, Human Liver tissue:
cloning vector is gtl1: "
a 56 c 58 g 105 t
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HSAAABDCI B, Human Liver tissue Homo sapiens cDNA, mRNA sequence.
2119960.1 GI:26705
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            3920 TITAATITAAATTAITGITAATAATAATAACATATAAGAATACTITITATTAAAATAACCAIG 3979
                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 329)
MRC Human Genome Mapping Project Resource Centre.

The UK-HGMP cDNA program
Unpublished (1993)
Contact: MRC Human Genome Mapping Project Resource Centre
Clinical Research Centre
Watford Road, Harrow, Middlesex HAl 3UJ,U.K.

Email: bindelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                Length 529;
                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 322; DB 38; Length 5
Best Local Similarity 100.0%; Pred. No. 2.4e-112;
Matches 322; Conservative 0; Mismatches 0; Indels
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On May 18, 1995 this sequence version replaced gi:811190.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Robert Strausberg(anh, gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CONA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:

www-bio.llni.gov/bbrp/image/image.html
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 529)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/dev_stage="adult"
/lab_host="bH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT773D
/note="Organ: parathyroid gland; Vector: pT773D
/site_2: Eco RI: 1st strand cDNA was primed with a Not I:
                         3670 TGTCCTTTTGTACCAGTCTGTAACTTAACTATAGTATAATGAAAAGAATGACCTATAATA 3729
                                                                                                                                                                                                                                                                              3730 TAGGTGTTTTGTAGATTCTTGTGTCACTGCAAACAATATGAACTCCTTTTTCGTATTGCC 3789
                                                                                                                                                                                                                                                                                                                                                               3790 ATCGGGTTGCATGGAAGTTTTATTCTCTTGTTTTGCTGGAAACCAAGAGGATCCAAACTT 3849
                                                                                                                                  209 TGTCCTTTTGTAGCAGTCTGTAACTTAACTATAGTATAATGAAAAGAATGACCTATAATA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 1133 Std Error: 0.00 Seq primer: -00m13 fwd. Er from Amersham High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1359653"
/clone_lib="Soares_parath
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AA772278.1 GI:2824061
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AA772278/c
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse.
Location/Qualifiers
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zu76a06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743890
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/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalla: Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalla: Butheria: Primates: Catarrhini: Hominidae: Homo.

I (bases 1 to 364)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra.M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washg-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 ITCAAGATGAAAGCTCTGTGCAGGCTCTCATTGATGCATTGAAGAAGATGGAAAAC 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 ICTACCTTTGTGTATCAAGTCCCACTATCAAGGATAAGCCAGTCCAGATTCGGCCTTGGA
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On Sep 12, 1996 this sequence version replaced gi:1393681.
Contact: Wilson RY
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302;
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Matches 302; Conservative
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AA634469/C
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Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 302)

1 (bases 1 to 302)

1 (bases 1 to 302)

8 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Flagarald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoglapaen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Badarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hung, J., Xu, C., Yu, G.L., Ruben, S.M., Kraser, C.M., and Venter, J.C., Engene, J.M., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Engene, J.M., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Engene, J.M., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Engene, J.M., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Engene, J.M., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
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                                                                                                                                                                                                           2887 GTGACGCAGTAGTCAGGCATCTTCACACCGACTTGAATATTGAAGTGCAGTTGTGTGGAA 2946
                                                                                                                                                                                                                                                                                                                 2947 CITGGATCATCTTAGTTGATTTTGTTTAAATTATGATTCCACATATGACAAAAATCCAGA 3006
                                                                                                                                                                                                                                                                                                                                                                                                                       3007 TCCACTAATTAAAATGAGGGTTTATGTCTATGAATAATCTCCTGTGGGTTTAATCTCATA 3066
                                                                                                                                     109 CITGGATCATCTTAGTTGATTTTGTTTAAATTATGATTCCACATATGACAAAAAATCCAGA 150
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                                                     Gaps
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12140200

On Sep 12, 1996 this sequence version replaced gi:1400776.

Other_ESTS: EST94220 THC177549

Contact: Kerlavage, AR

Bioinformatics
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  Length 329;
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9712 Medical Center Drive, Rockville, MD 20850 USA
7e1: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
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Nature 377 (6547 Suppl), 3-174 (1995)
                                                     Indels
7.5%; Score 320; DB 20; L ilarity 100.0%; Pred. No. 1.7e-111; Conservative 0; Mismatches 0;
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AA381126.1 GI:2033496
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us-09-090-672b-1.oligo_1.rst

9

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On Dec 20, 1995 this sequence version replaced gi:1131028.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: 1011 496-1550

Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmetr-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CON Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: lung: Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 rolons made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA782211 274 bp mRNA EST 31-DEC-1998 ai47h12.s1 Soares_parathyroid_tumor_NbHPA Homo saplens cDNA clone 1360199 3', mRNA sequence.
    1 (bases 1 to 395)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soares and M. Fatima Bonaldo.
58 c 61 g 146 t
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/db_xref="taxon:9606"
/clone="INAGE:22751"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH109"
                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -400P from Glbco.
Location/Qualifiers
1. .395
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AA782211.1 GI:2841542
                                                                  Tumor Gene Index
Unpublished (1997)
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AA782211/c
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                                                                                                                          /organism="Homo sapiens"
/db_xref="Taxon:9606"
/clone_lib="Soares_testis_NHT"
/sex="mine"
/lab_nost="DH10B"
/note="Vector: p1773D-pac (Pharmacia) with a modified
/note="Vector: p1773D-pac (Pharmacia) with a modified
/note="Vector: p1773D-pac (Pharmacia) with a modified
/lab_nost="Income libe" (Pharmacia) with a modified
/lab_nost-libe" (Pharmacia) with a modified
/lab_nost-libe (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                                                                           AI802170 395 bp mRNA EST 06-JUL-1999
tx25b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270571 3',
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd Er from Amersham High quality sequence stop: 299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3898 AAACAATAGAGTATTTTGGGTTTTTAATTAATTATTGTTAATATATATAACATATAAGAA 3957
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 244; DB 36;
Pred. No. 1.2e-82;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRNA sequence.
AI802170
AI802170.1 GI:5367642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.78;
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/ Organism="Homo sapiens"
// Ab_xref="taxon:9606"
// Ab_xref="taxon:9606"
// Clone="IMAGE:1518146"
// Clone="IMAGE:1518146"
// Ab_host="Delomyosarcoma"
// Inb_host="Delomyosarcoma"
// Inbarnacia), Glagested with Not I and cloned into the Not I and Eco RI sites of the modified pt773 vector. Library
// Went through one round of normalization. Library
// Went through one round of normalization. Library
// Constructed by Bento Soares and M. Fatima Bonaldo."
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AA417896 AA417896.1 GI:2079715 human.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2.1 to 2.
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On Sep 12, 1996 this sequence version replaced gi:1398114.
Contact: Robert Strausberg, Ph.D.
Tral: (301) 496-1550
Enail: Robert Strausbergenin.gov
unknown library type
Enail: Robert Strausbergenin.gov
unknown library type
Enail: 40m13 fwd. ET from Amersham
High quality sequence stop: 178.
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4.5%; Score 191; DB 39; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-62;
Matches 191; Conservative 0; Mismatches 0; Indels
                  mRNA sequence.
AA903370
AA903370.1 GI:3038493
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IE 1 (bases 1 to 274)

NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Sep 29, 1997 this sequence version replaced gi:1520658.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 46-1550

Email: Robert Strausberginh.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 1172 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 253.
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4.5%; Score 193; DB 38; Length 274;
Best Local Similarity 100.0%; Pred. No. 38-63;
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Trevaskis E., Waterston, R., Williamson, A., Wohldmann, P. and
Trevaskis E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Werck EST Project
The Unpublished (1995)
Contact: Wilson SK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1810
Email: esfewatson.wustl.edu
Insert Size: 337
High quality sequence stops: 289 Source: IMAGE Consortium, LLNL
High quality sequence stops: 289 Source: IMAGE Consortium, CLINL
High quality sequence stop: 289.
Insert Length: 937
Seq primer: T3
High quality sequence stop: 289.
Insert Length: 937
High quality sequence stop: 289.
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Bukaryota, Metazoa, Chordata: Craniata; Vertebrata, Mammalla, Eukaryota, Metazoa, Catarrhini; Hominidae; Homo.

Li (bases I to 38 to 18 
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4.4%; Score 187; DB 21; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.1e-61;
Matches 187; Conservative 0; Mismatches 0; Indels (
                                                                          GI:727140
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/clone="inade:752772"
/clone=lib="Soares=NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/tasue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201);
Sis Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kirzman,D., Nucaba,T., Lacy,M., Leb. N., Lennon,G., Marra,M., Martin,J., Morce,B., Schellenberg,K., Steptoe,M., Tan,F., Theising B., White,Y., Wylie,T., Waterston,R. and Wilson,R. unpublished (1997)

On Sep 12. 196 fils sequence version replaced gi:1393055.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286
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Best Local Similarity 100.0%; Pred. No. 2.7e-61;
Matches 188; Conservative 0; Mismatches 0; Indels (
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Experiments of the context of the 
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EST94220 Activated T-cells I Homo sapiens cDNA 3' end, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoc RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NDHDU, and fetal heart NBHHMJW) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization this DNA saction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools of 34048-459, and 484488-489479."
                                                                                                                                                                                                                                                              Entaryota Mammalia; Entartora; Craniata; Vertebrata; Mammalia; Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.

Entheria: Primates; Catarrhini; Hominidae; Homo.

Entheria: Primates; Catarrhini; Hominidae; Homo.

Nor.GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.

Tumor Gene Index.

Tumor Gene Index.

Transbergen; Ph.D.

Contact: Robert Strausbergen; Ph.D.

Tel: (301) 496-1150

Tel: (301) 496-1150

Tel: (301) 496-1150

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lnn.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham

High quality sequence stop: 339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
A1093858 365 bp mRNA EST 18-AUG-1998
qa30dO5.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1688265
3', mRNA sequence.
A1093858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Organism="Homo sapiens"
/Organism="Homo sapiens"
/Obstate="taxon:9606"
/Clone="INAGE:168255"
/Clone="Ib="Soares_NhHMPu_S1"
/Lissue_Type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4194 AATTAATTTTCAGGGTTTTGAGGCTGAACATAATTTCATTATCCCTCAAAAGGTTACCAC 4253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4074 TCTCTCTCTTTTTTCCATCCTTTTTAATTTTTTAACAGCAATGGAGGAGGAGGTTAACAAT 4133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 TCTCTCTTTTTTCCATCCTTTTTAATTTTTTTAACAGCAATGGAGGAAGTAACAAT 127
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                                                                                                                                                                           AI093858.1 GI:3432834
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Best Local Similarity 100.C
Matches 186; Conservative
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ORGANISM
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ACCESSION H57530 VERSION KEYWORDS EST. SOUNCE ONGANISM EMATOR Herazoa; Chordata; Craniata: Vertebrata; Mammalia; Etheria; Primates; Catarrhin; Hominidae: Homo. EUNaryota; Metazoa; Catarrhin; Hominidae: Homo. EUNaryota; Primates; Catarrhin; Hominidae: Homo. EUNaryota; Primates; Catarrhin; Hominidae: Homo. REFERENCE 1 (bases 1 to 410) AUTHORS Hillier, L. Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Parsons, J., Rifkin, L., Rohlfing, T., E.M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Marck EST Project JOURNAL Unpublished (1995) COMMENT On Jan 24, 1995 this sequence version replaced g1:634282.	Washington Onlyesity School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: est/ewatson.wustl.edu Insert Size: 902 High quality sequence stops: 361 Source: InAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Insert Length: 902 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 361. FEATURES Source Location/Qualifiers Source	/Organismi - Now Sapless / Ob_Xref="Lexon:9606" / Ab_Xref="Lexon:9606" / Ab_Aref="Lexon:9606" / Ab_Aref="Lexon:9606" / Ab_Aref="Lexon:9606" / Sex="male" Soares fetal liver spleen INFLS" / Sex="male" Soares fetal liver spleen INFLS" / Ab_Ast="Dalba" (amplicitud nesistant) / Ab_Abst="Dalba" (amplicitud nesistant) / Ab_Abst="Dalba" (amplicitud nesistant) / Ab_Actgand (application fetal liver spleen; Vector: pr773D (Pharmacia) / Ab_Actgand (application fetal liper spleen; Vector: pr773D (Pharmacia) / Ab Actgand (application fetal liper spleen; Vector: pr773D (Pharmacia) / Ab Actgand (application fetal liper spleen; Vector: pr773D (app	and Eco R 1 sites of the modified piTr3 vector. Library went through one round of normalization. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." EASE COUNT 97 a 79 c 116 g 115 t 3 others ONEGIN 3.3%; Score 140; DB 23; Length 410; Best Local Similarity 100.0%; Pred. No. 3.5e-43; Matches 140; Conservative 0, Mismatches 0, Indels 0, Gaps 0;	575 TACGCTGGGATTGATACCGACCCTGAGCTAAAATACCCCAAAAGGAGCTGGGAGAGTTGCG 634 11111111111111111111111111111111111	DD 290 GUAGAGAATAAACGGGT 309 RESULT 17 AQ883641/C LOCUS AQ883641 559 bp DNA GSS 09-NOV-1999
Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 156) Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, LI., Marmaros, S.M., Morrick, J.M., Noreno Palanques, R.E., Scott, J.L., Saudek, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Drimke, D., Feng, D.P., F., Richer, J., Hudson, P., Kim, A.K., Brank, D. L., Kands, D. F., Greene, J.M., Gruber, J., Hudson, P., Brank, D. L., Kandsch, C., Lin, S., Cleman, T.A., Collins, E.J., Brank, D. L., Kandsch, C., Lin, Gruber, J., Hudson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, S., Clemen, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Meisson, P., Brank, D. L., Kandsch, C., Lin, J., Li, M., Brank, D., Brank, D. L., Kandsch, C., Lin, J., Li, M., Brank, D., Brank, D. L., Kandsch, C., Lin, J., Li, M., Brank, D., Brank, D. L., Kandsch, D., Li, Li, Li, Li, Li, Li, Li, Li, Li, Li	TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million ucleotides of CDNA sequence based upon 83 million nucleotides of CDNA sequence based upon 83 million nucleotides of CDNA sequence based upon 83 million nucleotides of CDNA sequence of	For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: Mi3-21. Seq primer: Mi3-22. Location/Qualifiers Location/Qualifiers 1. 156 /Organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone_lib="Activated T-cells I" /cell_type="T-lymphocyte" /dev_stage="adult" /hote="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: whore"	BASE COUNT 43 a 28 c 25 g 60 t ORIGIN ORIGIN 3.6%; Score 156; DB 33; Length 156; Best Local Similarity 100.0%; Pred. NO. 4.2e-49; Natches 156; Conservative 0; Mismatches 16; Op. 4.106 TTTAACAGCAATGGGAAGTTAACAATTTTAATGGAAAGAGCATGTTAGAGCAAACAA 4165 Qy 4106 TTTAACAGCAATGGAAGTAACAATTTTAATGGAAAGAGCATGTTAGAGCAAACAA 4165	.56 TITAACAGCAATGGAAGTTAACAATTITAAIGGAAAGACCATGTTAGAGC 166 AIGCATAAGCAAGACTGAACATTATTAAITTCAGGGTTTTGAGGCTG 1111111111111111111111111111111111	KESSUZT 16 H57530 H57530 410 bp mRNA EST 05-OCT-1995 LOCUG DEFINITION yr05bl0.r1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA clone IMAGE:204379 5' similar to SP:C40HI.1 CE00109 OVARIAN PROTEIN ;, mRNA sequence.

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/ Organism="Homo sapiens"

/ Organism="Homo sapiens"

/ Ob_xref="cob:467860"

/ Clone="Lib="coares fetal liver spleen lNFLS"

/ Clone="Lib="Soares fetal liver spleen lNFLS"

/ Clone="Lib="Coares fetal liver spleen lNFLS"

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                                      clone
      T95805 304 bp mRNA EST 17-MAR-1995 yd56d10.r1 Soares fetal liver spleen 1NFLS Homo sapiens CDNA clon IMMGE:112243 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 AGATGGAAAACTCTACCTTTGTGTATCAAGTCCCACTATCAAGGATAAGCCAGTCCAGAT 423
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  Homo sapiens

Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Mammalia Bukaryota; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 304)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R.
The WashU Marck EST Project
Uppublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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ilarity 100.0%; Pred. No. 2.5e-39;
Conservative 0; Mismatches 0;
                                                                                             mRNA sequence.
185805
185805.1 GI:714157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3618
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleter@dejong mad.buffalo.edu). Clones may be purchased from BACPG Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 9246 row: F column: 22
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 559)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. (Nall. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3149 AAAAAAATGTAAAATGATAGATAATAAAAGCCTTACTAGGTTCTTAAAAGATGAACTATC 3208
HS_5478_B2_C11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9246 Col=22 Row=F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GTAGACTCTTATTTTTGATTGCAGGTGGAAGTTAAGCCATATGTCTTGGATGATCAGCTG 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 135; DB 88; Length 559; Similarity 99.0%; Pred. No. 2.4e-41; S. Similarity 99.0%; Mismatches 3; Indels 5; Conservative 0; Mismatches 3; Indels
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/db_xref="taxon:9606"
/db_xref=plate=9246 Col=22 Row=F"
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/sex="male"
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Location/Qualifiers
1. .559
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                                      AQ883641.1 GI:6315108 GSS.
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T85805
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QQ ð ρp ò Dp ò Db ò 13

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 764)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mark Madma

Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research Genetics (info@resgen.com). BAC
The Institute for Genomic Research Genetics (info@resgen.com). BAC
The Institute for Genomic Research for Genomic Genomic Research for Genomic 
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa 1 to 639)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ744981 764 bp DNA GSS 16-JUL-1999 HS_5501_A2_C03_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1077 Col=6 Row=E, genomic survey sequence. AQ744981. GI:5522591
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/sex="Male"
/sex="Male"
/cell_type="Sperm"
/note="Sector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%; Score 53; DB 81: Length 639; Best Local Similarity 100.0%; Pred. No. 3.2e-10; Matches 53; Conservative 0; Mismatches 0; Indels
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High Throughput Sequencing Center
University of Washington
401 Ouean Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3518
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:5379185"
/db_xref="taxon:9606"
/clone="386K14"
                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Other_GSSs: CIT-HSP-386K14.TF
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1. .639
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Anote—"Organ: pooled; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Ibraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries The pools consisted of the following libraries and clonelDs: Scares NBSRP pool 1: 309384-310919, 33208-325895 Scares NBSRP pool 1: 145032-14735, 147720-148103, 148872-149255, 15002 - 150407, 151176-15237 Scares NBPRR-9W pool 1: 304776-30631, 772104-774407 Scares NBHPA pool 1: 7321204-774407 Scares NBHPA pool 1: 732120-726407, 739080-740999 Subtraction by Bento Scares and M. Fatima Bonaldo." 1 others
                                                                                                                                                                                                                                                                                                            Entaryota sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Petarrhini; Hominidae; Homo.
E 1 (bases 1 to 568)
S NGT-GAB http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
I Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187416.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is avaliable royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality sequence stop; 483.
I contact: Management of the Contact of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                            AI762436 568 bp mRNA EST 24-JUN-1999 wg57a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369168 3', mRNA sequence.
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B55278
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/db_xref="taxon:9606"
/clone="IMAGE:2569168"
/clone=lib="Scares_NSF_F8_9W_OT_PA_F_S1"
/lab_host="DH108"
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AI762436.1 GI:5178103
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B55278.1 GI:2609612
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Gaps

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Contact: Kerlavage, AR
Bioinformatics
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Fox: 3018699423
Fox: 3018699420
Fox: 301869420
Fox: 3018699420
Fox: 3018696420
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa 1 to 269)

Adams, M.D., Kerlavage, A.R., Fields, C. and Venter. J.C.

3,400 expressed sequence tags identify diversity of transcripts from human brain

Nature Genet. 4, 256-267 (1993)

93364420

on Sep 12, 1996 this sequence version replaced gi:1407373.

Other_ESTs: THC83368
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EST58017 Infant brain Homo sapiens CDNA 3' end similar to EST
AA350648 GI:2002965
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Matches 46; Conservative 0; Mismatches 0;
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Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-II. For BAC
Clones are derived from the human BAC library RPCI-II. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1077 row: E column: 6
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 764.

/clone_ity sequence stop: 764.
/clone_ity raxon:9666"
/clone_ity raxon:9666"
/clone_ity late-ity rol-6 Row-E"
/clone_ity=RPCI-II Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Adams, M.D. Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, R., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
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clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /carw_male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
a 138 c 164 g 228 t l others
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/sex="Male"
/cell_type='Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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1.1%; Score 47; DB 87; Length 76
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 47; Conservative 0; Mismatches 0; Indels
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Other_GSSs: CIT-HSP-234805.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 261
/organism="Homo sapiens"
/db_xref="taxon:9606"
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The WashUrberck EST Project
The WashUrbished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tal: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 926
High quality sequence stops: 203 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
Insert Length: 926
Seq primer: M13RP1
Seq primer: M13RP1
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                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-388
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2124 row: D column: 18
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2124 Col=18 Row=D"
/slone=Ib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: sperm: Vector: pBeloBAC11: BAC Clones in E-Coli DH10B" 2 others
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 426)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Socaes,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                     Tumor Gene Index
In Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151892.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausbergfaih, gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Narayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Bukaryotas Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 434)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                             Home sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Mammalia;
Eutheria: Primates; Catarrhini: Hominidae; Homo.
1 (bases I to 343)
MCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap;
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 2046 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon.9606"
/clone="IMAGE.1591347"
/clone_lib="NCI_CGAP_Kid6"
     repetitive element ;, mRNA sequence.
AA955031
AA955031.1 GI:3118726
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AQ608513
AQ608513.1 GI:5068507
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Les 46; Conserv
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                                                                                                       human.
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AQ608513/c
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Exax: 301 838 0200
Email: mdddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1to 602)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.G.
Use of a random BAC End Sequence Database for Sequence-Ready Map
/clone_lib="RPCI-11"
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/note="Vector: pBAc63.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
1 126 c 106 g 181 t
                                                                                                                                                                                                                                                                                                                                                                                            B58317 602 bp DNA GSS 20-JUN-1998 CIT-HSP-2012I14.TR CIT-HSP Homo sapiens genomic clone 2012I14, genomic survey sequence.
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/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 44; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 9e-
tive 0; Mismatches
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Unpublished (1997)
Other_GSSs: CIT-HSP-2012I14.TF
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B58317.1 GI:2612651
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Best Local Simi
Matches 44;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhin; Hominidae; Homo.

I (Pases I to 534)

S Lado, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building

Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(Pieter@dejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@fresgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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RPCI11-144G16.TJ RPCI-11 Homo Sapiens genomic clone RPCI-11-144G16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 426
/organism="Homo sapiens"
/db.xref="GDB:565482"
/db.xref="taxon:9606"
/clone="INAGE:153190"
/clone=lib="Soares breast 2NbHBst"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7555071"
/db_xref="taxon:9606"
/clone="RPCI-11-144G16"
  High quality sequence stop: 203.
Location/Qualifiers
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AQ388631
AQ388631.1 GI:4359654
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LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

RESULT 29 AA654395

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Turnor Gene Index

Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3137633.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausbergenin, gov.

Tel: (301) 496-1550

Email: Robert_Strausbergenin, gov.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.,

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40Up from Gibco
High quality sequence stop: 375.

Location/Qualiflers
1. 383
Ab_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="NoI_GAP_Gas4"
/clone=lib="NoI_GAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/hab_host="DH10B"
/note="Organ: stomach: Vector: pCMV-SPORT6; Site_1: Salt: Site_2: NoII; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zn55909.rl Stratagene fetal retina 937202 Homo sapiens CDNA clone
IMAGE:565984 5' similar to contains Alu repetitive element; contains
element MER22 repetitive element; , mRNA sequence.
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1 (bases 1 to 391)
Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohiling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 383) NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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100.0%; Pred. No. 2.4e-06;
tive 0; Mismatches 0;
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AA121819.1 GI:1679469
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Best Local Similarity 100.0
Matches 43; Conservative
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  Homo sapiens
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Eutheria: Primates: Catarrhini: Hominidae: Homo.

I (Dasses 1 to 180)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

I unpublished (1997)

On Sep 19, 1997 this sequence version replaced gi:1520479.

Contact: Robert Strausberg@nih.gov

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones.

Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Arrayed by: Greg Lennon, Ph.D.

My Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Mark Raffeld, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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3.3e-06; Indels
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FEATURES

RESULT 30 A1926033

BASE COUNT

DEFINITION

ACCESSION

VERSION KEYWORDS

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Gaps

Gaps

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MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
Am Klopferspitz 18a D-82152 Martinsried, Germany
The 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; Site_1: NotI; Site_2: SalI/MluI"
143 t
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This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY: Email: clone@trzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                   Genomic sequence of BAC ends"
8 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALO47553 470 bp mRNA EST 29-SEP-1999 DKFZp586E0121_s1 586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586E0121, mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST (Ottenwaelder, et al.)
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189405.
Contact: Ottenwaelder B
                                                                                                                                                                                                                                                                                                                                                                    Length 406;
                                                                                                                                                                                                    /clone_lib="RPCI-11 Human Male BAC Library" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 470;
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/db_xref="taxon:9606"
/clone="Nbxzpp86E0121"
/clone_lib="586 (synonym: hutel)"
/tissue_type="uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 CICTGCCTCCCGGGTTCAAGTGATTCTCCTGCCTTAGCCTCCC
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2.4e-06;
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                                                                                                                                                            /db_xref="taxon:9606"
/clone="Plate=811 Col=2 Row=1"
                                                                                                                                                                                                                                                                                                                                                 1.0%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Ger
92 c 85 g 148 t
                                                                                         Location/Qualifiers
1. .406
/organism="Homo sapiens"
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108 c 94 g 14
       Plate: 811 row: I column: 2
Seq primer: T7
Class: BAC ends
High quality sequence stop: 406.
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/lab_host="DH10B"
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AL047553.1 GI:4728549
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Best Local Similarity 100.0
Matches 43; Conservative
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3818
Fax: (206) 616-382
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
http://www.htsc.washington.edu
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I bases 1 to 40.
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 28M13 rev2 from Amersham
High quality sequence stop: 240.
Location/Qualifiers
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HS_5235_A2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=811 Col=2 Row≠I, genomic survey sequence.
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97044478
On May 5, 1995 this sequence version replaced gi:798452.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Matches 43; Conserv
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I thases; I to 40. Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="laxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBACI1; BAC Clones in
F-Coli DH10B"
100 c 87 g 77 t 2 others
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                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Scanning the human genome
L Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
E 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-382
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3237 row: B column: 12
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3237 row: H column: 10
Class: BAC ends
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100.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 0;
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Location/Qualifiers
1..389
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Matches 41; Conserv
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                                                  Hood, L.
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AQ206027/c
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Unsure of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: bbe@tign.org
Clones are available from Research Genetics (info@resgen.com). BAC
ends search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3.21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 527)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
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HS_2237_B2_A06_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3237 Col=12 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calrech Human BAC Library D"
                                                                                                                                                                    AQ394316 527 bp DNA GSS 06-MAR-1999 CITBL-E1-2546J9.TF CITBL-E1 Homo sapiens genomic clone 2546J9, genomic survey sequence.
AQ394316.1 GI:4365339
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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       1894 CAACCTCTGCCTCCCGGGTTCAAGTGATTCTCCTGCCTTAGC 1935
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1.0%; Score 42; DB 102;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 42; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="2546J9"
/clone_lib="CITBI-E1"
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1. .527
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AQ205998/c
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AQ394316/c
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154 CTGCCTCCCGGGTTCAAGTGATTCTCCTGCCTTAGCCTCCC 114
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AQ742061/c
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3868
Email: jwallacequ washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3222 row: J column: 24
Seq primer: T7
Class: BAC ends
High quality sequence stop: 513.
Location/Qualifiers
1. 513
//organism="Homo sapiens"
//organism="Homo sapiens"
//clone="Plate=3222 Col=24 Row=J"
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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 1. .400
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Piate=3237 Col=10 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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                                                                                                          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 89 9 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ763211 513 bp DNA GSS 28-JUL-1999 HS_3222_B2_E12_T7C CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3222 Col=24 Row=J, genomic survey
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1.0%; Score 41; DB 99; Length 40
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 41; Conservative 0; Mismatches 0; Indels
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AQ763211.1 GI:5641327
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AQ763211/C
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701: (206) 616-3868
Fax: (206) 616-3868
Fax: (206) 616-3868
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
11brary avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1146 row: P column: 24
                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 693)
Mahairas,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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RPCIII-7317.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-7317,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
AQ742061 693 bp DNA GSS 16-JUL-1999
HS_5570_B2_H12_SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1146 Col=24 Row=P, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
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100.0%; Pred. No. 1.1e-05;
Live 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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Location/Qualifiers
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AQ268072.1 GI:3795676
                                                                                         AQ742061
AQ742061.1 GI:5519583
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Best Local Similarity 100.
Matches 41; Conservative
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Class: BAC ends
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1900 CIGCCICCGGGTICAAGIGATICICCIGCCITAGCCICCC 1940

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/tissue_type="retina"
/dev_stage="fetina"
/dev_stage="55 year old"
/lab_host="bluob (ampicini profile in the incomplete i
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Euthoria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 30).
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the INSAC Consortium (info@image.llnl.gov) for further information.
INSAC Length: 2948 Std Error: 0.00
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 230.
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
1911: (206) 616-3887
Eax: (205) 616-3887
Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="CDB:1288453"
/db_xref="taxon:9606"
/clone="IMAGE:380196"
/clone_lib="Soares retina N2b4HR"
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Pred. No. 9.2e-05;
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AQ100978.1 GI:3472007
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                          Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Contact: Mark Adamsotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The 11: 301 838 0200
Fax: 301 838 0209
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1 (bases 1 to 274)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Haukins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Homo,B., Morlis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schallenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please confect Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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2f48e07.rl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:380196 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
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RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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On May 5, 1995 this sequence version replaced gi:797877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 104;
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   Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00013;
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Washington University School of Medicine
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100.0%; Pred. No. v.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7527846"
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AA054055.1 GI:1544979
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Best Local Similarity 100.
Matches 39; Conservative
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SOURCE

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FEATURES

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/esc."male"
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/fab_host="pH10B (a
H84675 132 bp mRNA EST 14-NOV-1995 y956604.r1 Soares retina N24HR Homo sapiens cDNA clone IMAGE:219751 5' similar to contains Alu repetitive element; ontains Alu repetitive element; mRNA sequence. H84675.1 GI:1063799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is and alable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
Insert Length: 1057 Std Error: 0.00
Seq primer: M13RPl
High quality sequence stop: 357.
Location/Qualifiers
L. 132
                                                                                                                                                                                                                                                                                                                                                     Gaps
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Dukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 132)
Hillier, L., Claark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, B., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                 0.9%; Score 38; DB 28; Length 115;
llarity 100.0%; Pred. No. 0.00031;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 1894 CAACCTCTGCCTCCGGGTTCAAGTGATTCTCCTGCCT 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:219751"
                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 38; Conserv
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H84675/c
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[ (bases 1 to 115)
Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Mordis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlign, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA084176 115 bp mRNA EST 31-JUL-1997
znl7d10.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
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On May 8, 1995 this sequence version replaced gi:801257.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Exa: 314 286 Exror: 0.00
Exa: 314 286 Exror: 0.00
Exa: 314 286 Exror: 0.00
Exa: 40M13 464 from Amersham
High quality sequence stop: 97.
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                                                                                                                                                                                                                                                                                                                                   /note="organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli PH10B" 79 9 80 t
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3. 8.9e-05;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 8.9 Matches 39; Conservative 0; Mismatches
   Sequence Tagged Connector
Plate: 3061 row: A column: 5
Class: BAC ends
High quality sequence stop: 301.
Location/Qualifiers
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AA084176.1 GI:1626358
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LOCUS
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Insert Length: 656 Std Error: 0.00
Seq primer: ~41ml3 fwd. ET from Amersham
High quality sequence stop: 155.

1. .157
Location/Qualifiers

1. .157
Location-Lib=NorDis

2. .157
Location-Lib=N
                                                                                                                                                                                                                                                 Tunor Game Index.

Tunor Game Index.

Unpublished (1997)

On Apr 14, 1993 this sequence version replaced gi:638990.

On Apr 14, 1993 this sequence version replaced gi:638990.

On Apr 14, 1993 this sequence version replaced gi:638990.

On Apr 14, 1993 this sequence version replaced gi:638990.

Tel: (301) 496-1580.

Email: Robert_Strausbergenin.gov.

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G. E. Consortium/LiNi at:

www-bio.llnl.gov/bbrp/image.html
                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Prinates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 157)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity
Matches 38; Conserv
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA908331 151 bp mRNA EST 13-APR-1998 og955066.si NCI_CGAP_OV8 Homo sapiens cDNA clone IMAGE:1454123 3, similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAP http://www.ncbi.nlm.nih.gov/ncicgap.
NoricGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2043584.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
unknown library type
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Gaps
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hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Falma Bonaldo. " 34 c 45 g 24 t.
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (Pases 1 to 151)
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/lab_host="DH10B"
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0.9%; Score 38; DB 24; I
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 38; Conservative 0; Mismatches 0;
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0.9%; Score 38; DB 40; I
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 38; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:1454123"
/clone=lib="NCI_CGAP_Ov8"
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AA908331.1 GI:3047736
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AA397419
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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VERSION
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TITLE
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AA908331
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Gaps ö

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Length 157; Indels

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24-MAY-1996; US-655360.
(GENZ ) GENZYME CORP.
Burn T, Connors T, Dackowski W, Germino G, Klinger K,
                                                          Oian F;
WPI; 98-018511/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of the normal human PKDI gene from The present sequence is that of the normal human PKDI gene from The present sequence is that of the normal human pKDI gene from The present sequence is that of sequence (a. transversions, deletions and/or insertions) are associated with a transversions, deletions and/or insertions is generally of the presence of the presence with a previously reported partial conversable). The most significant difference is the presence of two additional cytosine residues on the plus-strand at position 4566 of the previously reported sequence. The insertion results in a frame-shift in the predicted protein coding sequence, calling to replacement of 92 C-terminal amino acids with a novel calling acid C-terminus. The PKDI gene contains 23 Alu repeats. The prepart and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp repeat and two large CT-terminal mopies of a perfect 27 bp and 250 mopies of a perfect 27 bp and 250 mopies of 250 mopi
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Human FDL locus between chromosomal markers ATPL (ATP6C) and D16S84.
Human: polycystic Atland disease 1; PKD1; treatment;
autosomal dominant polycystic kidney disease; APKD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polycystic kidney disease gene and its mutants - useful for treatment of polycystic kidney disease and screening for
                                                                                                         Location/Qualifiers
4379. .5272
4379. .ft.ag.
4379. .ft.ag.
4379. .ft.ag.
4370. .ft.ag.
 1885 CICACIGCAAGCICCGCCICCTGGGITCACGCCAITCICCTGCCTCAGCCICC 7937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 53577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connors TD, Dackowski W, Germino G, Klinger KW;
, Qian F;
                                                                                                                                                                                                                                                                                                                                      /*tag= d
/note= "insertion, results in frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                             /*tag- c //note- replaces Val codon by Leu codon lnsert(51827 .51828, cc) /*tag- d /*tag- d
                                                                                                                                                                                                                        /*tag= b
/note= "changes Val_codon to Leu codon"
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1.8%; Score 53; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.4e-11;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            replace(50796. .50797, cg)
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31-7AN-1995; US-381520.
(IGIG-) IG LAB INC.
(UXJO) UNIV JOHNS HOPKINS.
Burn TC, Connors TD, Dack
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22-MAY-1997; U08799.
03-JUN-1996; US-658136.
                                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-1995; Ul3357
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WO9744457-A1.
                                                                                                                                                                                                                                                                                                                                                                       WO9612033-A1.
                                                                                           Homo sapiens
                                                                                                                                 misc_feature
                                                                                                                                                                                                       old_sequence
                                                                                                                                                                                                                                                              ojd_sequence
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T94108
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Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease.

Example 5; Pages 60-89; 257pp; English.

The present sequence is the human polycystic kidney disease 1 (PKD1) locus between chromosomal markers ATPL (ATP6C) and D16S84.

The PKD1 gene or polypeptide may be used to treat autosomal cominant polycystic kidney disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and
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The 1.5 kbp region from the EcoRI to the PstI site shows the region of homology in the human erbB-3 gene. The region contains 3 ORFs. See Q12224 for full erbB-3 gene. 333 C; 387 G; 359 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ë
                                                                                                                                                                                                                                                                                                                                                                        antisense sequences derived from the PKD1 gene may used for detection and therapy.

Sequence 53577 BP; 8495 A; 17684 C: 15707 C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-5EP-1991 (first entry)
BrbB-3 gene clone E3-1 v-erbB homologous region.
Epidermal growth factor; EGRF; receptor; erbB; antibodies; tumour;
v-erbB; probe; ss.
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WPI; 91-193144/26.
P-PSDB; R12607.
Epidermal growth factor receptor related gene - used for
producing receptors and antibodies for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 53577;
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100.0%; Pred. No. 2.7e-10;
tive 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 6.4e-11;
nes 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
66. .221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q12223/c
ID Q12223 standard; DNA; 1474 BP.
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(USDC ) US SEC OF COMMERCE.
(USSH ) NAT INST OF HEALTH.
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657. .855
/*tag= b
973. .1446
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Best Local Similarity 100.0
Matches 52; Conservative
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30-NOV-1990; U07025.
01-DEC-1989; US-4444
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Matches
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64 CACTGCAAGCTCCGCCTCCTGGGTTCACGCCATCTCCTCGCCTCAGCCTCCC 115

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Gaps

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is useful for controlling bacterial infection and unlike chicken lysozyme HL has little adverse effects. Sequence 1496 BP; 443 A; 299 C; 308 G; 446 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erbb-3 genomic sequence.
erbb-3, antibody; proto-oncogene; cancer; receptor tyrosine kinase;
tumour; diagnosis; ss.
                                                                                                                                                                                                                                         140 GCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGACAGGGTTTCACC 191
                                                                                                                                                                                                                                                                890 GCCACCACCACCAGGGTAATTTTTTTTTTTAGTAGAGACAGGGTTTCACC 941
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1.7%; Score 52; DB 1; Length 1496;
Best Local Similarity 100.0%; Pred. No. 2.76-10;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.7%; Score 52; DB 1; Length 154 Best Local Similarity 100.0%; Pred. No. 2.6e-10; Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-1996.

04-DEC-1989; 444406.

04-DEC-1999; US-444406.

10-NOV-1992; US-978895.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

AALONSON SA, KRAUS MH;

WPI; 96-068302/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
66. .221
/*tag= a
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222 . 779
7*tag- b
778 . 855
7*tag- c
856 . 1039
7*tag- d
1040 . 1185
/*tag- e
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ID V58735 standard; cDNA; 1542 BP.
AC V58735;
                                                                                                                                                                                                                                                                                                                                                                                        110060/c
ID 110060 standard; DNA; 1542 BP.
AC 110060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-1996 (first entry)
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1542 BP; 389
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New DNA sequence -
encoding signal peptide and mature protein of human lysozyme
Figura 2-1 - 2-1; pages 12-13; 13pp; Japanes.

Tit is useful for effective expression of human lysozyme in yeast or
animal cells. Also, DNA encoding various proteins can be linked to the
3' end of the HL signal peptide, so that it is downstream of the
promoter of the expression vector. Expression of such proteins is
promoter of the expression vector. Expression of such proteins is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lysozyme gene -
useful promoter for genetic expression of animal culturing cell
useful promoter for genetic expression of animal culturing cell
i. Fig 4-1 to 4-3 Pages 834-835; 13pp; Japanese.
Human lysozyme DNA can be used to obtain transgenic animals, e.g. mice.
It can also be produced by culturing animal cells, and it can
promote the genetic expression of these animal cells.
Sequence 1494 BP; 441 A; 298 C; 309 G; 446 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1990 (first entry)
DNA coding for the signal peptide and mature protein of human lysozyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 1.7%; Score 52; DB 1; Length 1494; Local Similarity 100.0%; Pred. No. 2.7e-10; Nes 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lysozyme; HL; bacterial infection.
Homo sapiens.
                                                                                                                                                                                                                                                                                       Location/Qualifiers
14. .67
/*tag= a
68. .460
/*tag= b
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                                                                                                                                                                            20-DEC-1990 (first entry)
Sequence encoding human lysozyme
Transgenic animal; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1988; 151106.
21-JUN-1988; JP-151106.
(TAKE) Takeda Chemical Ind KK.
WPI: 90-053916/08.
P-PSDB; R06108.
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16-SEP-1987; 229752.
16-SEP-1987; JP-229752.
(TAKE) Takeda Chemical Ind KK.
                                                                                                                                    Q03369 standard; DNA; 1494 BP
Q03369;
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N92386;
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68..457
/*tag= b
14..460
/*tag= c
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Query Match Best Loca Matches

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DDICNPA
LOCUS
DEFINITION
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ORIGIN
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TITLE
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KEYWORDS
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Mooptera: Endopterygota; Lepidoptera; Glossata;
Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Hyalophora.

1 (bases 1 to 2431)

1 (bases)

1 (bases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTERLINGLGSIPEFSWYSPIKTGTYPLMTSYTYPPAQRPENYNHASYRNYBALREL
DIFEKTYOSLQKGOFESKKKIDEBRAIREYGKWYGRADLGGESTYKDVOGSYSY
IVAHHVLGAAPREDKHIFENGALDFYOTALADPAFYOLYNETYGYTUNERHYLLYPY
GEKLHFYGWKINDVYVEKLYTFFEYTEFDAINGYFWTEKEIKNSYPHNFKYROPRIN
KSENWINTEYKEDYATDAYLKIPMGRYDDNGFPILLEENWRYFFELLMFTHKITPGQN
KYBNNETLIRENSLYPLIDLKLLDEGKYPFDMSEEFGYMPKRLALPRGTFGGYP
GFFVFYPPESSSHDLIPFEAFYIDNRPLGYPFDRSEEFGYMPKRLALPRGTFGGYPFG

    10. .2124
    note-"hemolymph aromatic amino acid rich storage protein;

                                                                                                                                                                                                                                                                                                                                                                                                       LFQDVDQVNVNDEYYKIGKDYDVEANIDNYTNKKAVEEFLKLYRTGYLFRYFEFSIFH
HKLREEAIALFHLFYYAKDFETFYKSAAFARVHLNEGQFLYAYYIAVIQRNDTHGFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPYEVY PQFFVNMDTTVRIYRTKMODGILHPTKAINYGIVKEEBHYVYYANYSNTFL
INNEEORLTYLTEDIGFNSYYYYFHSHLPFWWTSERYGNLKHRGEIYYYFYOOLLTR
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YAALOPHORA cecropia moderately methionine rich hexamerin precursor,
mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MKTVLVLAGLIALVQSSVVSPVAHHYKTKDVDAVFVERQKKVLS
Veterinary School, 3800 Spruce Street, Philadelphia, PA 19104-6008,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58. .2121 /note="N-terminal sequence of the mature protein in the blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 32; DB 35; I
100.0%; Pred. No. 1.1e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  /product="arylphorin precursor"
/protein_id="AAB86644.1"
/db_xref="GI:2625146"
                                                                                            /organism-"Hyalophora cecropia"
/db_xref-"axon:7123"
/tissue_type-"fat body"
/dev_ztage-"5th instar larva"
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/product="arylphorin"
482 c 414 g (
                                                                                                                                                                                 /product-"arylphorin"
10. .2124
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Massey, H.C. Jr. and Telfer, W.H.
                                                     Location/Qualifiers
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Best Local Similarity 100.0
Matches 32; Conservative
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REFERENCE
AUTHORS
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TITLE
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JOURNAL
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AF032398
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KEYWORDS
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Direct Submission
Submitted (03-MOV-1997) Pathobiology, University of Pennsylvania
Veterinary School, 3800 Spruce Street, Philadelphia, PA 19104-6008,
USA
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/note-"alternate form of the mature protein in the blood"
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Dlotyosellum discoldeum cyclic nucleotide phosphodiesterase gene,
complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32. 2290
/note-"moderately methionine rich fat body storage
                                                                                                                                                                                                                                                                                                                                                                                                     /product="moderately methionine rich hexamerin"
32. .2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="allesture" --- | /note="allesture" | /noteduct="moderately methionine rich hexamerin" | /product="moderately methionine rich hexamering rich hexame
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/product="moderately methionine rich hexamerin"
6. 2287
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    2431
    /organism="Hyalophora cecropia"
    /db_xref="taxon:7123"

                                                                                                                                                                                                                                                                                                             /tissue_type="fat body"
/dev_stage="5th instar larva"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy 2245 TTTATTTAAAAAAAAAAAAAAAAAAAAAAA 2276
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SLINEEKKNIKTEGGSDNSEPSTEGELTGGATTKPGQQAGSALEGDSVQAQAQEGKQA
OPPVEPVPDEAKAQVPTPAPVNKNERNSKLINSLINSLINTSTSLINSSISLEKTILSTSTSK
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                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14.APR-1989) Myler P.J., Seattle Biomedical Research
Institute, 4 Nickerson Street, Seattle WA 98109-1651, U S A
2 (bases 1 to 7038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide and deduced amino acid sequence of the gp195 (MSA-1) gene from Plasmodium falciparum Palo Alto PLF-3/B11 Nucleic Acids Res. 17 (13), 5401 (1989)
                                       X15063.1 GI:9896
antigen: glycoprotein: gp195 gene; surface antigen.
malaria parasite P. falciparum.
plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 7038)
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2 (sites)
Faure, M., Franke, J., Hall, A.L., Podgorski, G.J. and Kessin, R.H.
The cyclic nucleotide phosphodiesterase gene of Dictyostellum
discoldeum contains three promoters specific for growth,
aggregation, and late development
Mol. Cell. Biol. 10 (5), 1921-1930 (1990)
90220576
On Mar 7, 1995 this sequence version replaced gi:167693.
Draft entry and computer-readable sequence for [Mol. Cell. Biol. (1989) In press] kindly provided
by R.H.Kessin, 23-MAR-1989.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels
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1163 . .6060
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t 3689. .6060
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3689. .4146
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BASE COUNT 2614
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intron TATA_signal

mRNA exon

REFERENCE AUTHORS TITLE

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JOURNAL MEDLINE COMMENT

FEATURES

TATA_signal

exon

ö Gaps ö Query Match 1.4%; Score 32; DB 34; Length 7038; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 32; Conservative 0; Mismatches 0; Indels 0

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PFGP195A 7038 bp mRNA INV 03-APR-1995 Plasmodium falciparum mRNA for major merozoite surface antigen gp195.

RESULT 25
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LOCUS
DEFINITION

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April 6, 2000, 09:00:38; Search time 345.99 Seconds (without alignments) 930.476 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-533-901B-1 US-08-839-032A-1 US-08-839-032A-1 PCT-US95-12724-1 PCT-US93-00227-2 US-08-776-944-13 US-07-920-281C-25 US-08-416-336-5 US-08-416-336-5 PCT-US94-05354-35 PCT-US94-05354-35 US-08-086-410-23 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-3 US-08-340-810-8	ENTS LAMMATORY . TO GMP-140	DB 7; . 2.6e- ches AAAAAAA 	Herpesvirus ereof ericas 0, Version ,566A
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	A NOT CAT	ari ons laaa	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
	7846 : MCI TIONE SEQ TION 110N	1.7%; Score 45; Similarity 100.0%; Pred. No. 5; Conservative 0; Mismat CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	A-1 Application US/08663: 5853733 FFORMATION: ATT: Macdonald, Richard: INVENTION: Recombing TINVENTION: and Uses FESQUENCES: 56 SUBERICA ADDRESS: SUBERICA ADDRESS: SUBERICA ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: SUBERICA ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: NUENCE ADDRESS: TING SYSTEM: FLORDY disk TYPE: Floppy disk TYPE: Ploppy disk TYPE: TYPE: Ploppy disk TYPE: TYPE: Ploppy disk TYPE: T
44 44 46 66 66 66 66 66 66 66 66 66 66 6	LT 1 464-1 ent No. 5378464 APPLICANT: MCEVER, RC TITLE OF INVENTION: A ADMINISTRATION OF GMP- NUMBER OF SEQUENCES: CURRENT APPLICATION NUMBER: FILING DATE: 08-MAI LENGTH: 2989	tch 1.7%; Score 45; DB 7; Len 45; Coll Similarity 100.0%; Pred. No. 2.6e-09; 45; Conservative 0; Mismatches 0; CCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	T 2 663-566-1 ent No. 585373 NERAL INFORMATION: APPLICANT: Goftran, MAR APPLICANT: Goftran, MAR TITLE OF INVENTION: Rec TITLE OF INVENTION: and NUMBER OF ENGURNESS: 5 CORRESPONDENCES: 5 CORRESPONDENCES: 5 CORRESPONDENCES: 6 CITY: New YORK STATE: New YORK COUNTRY: New YORK COUNTRY: New YORK COUNTRY: NEW YORK COUNTRY: NEW YORK CONTRY: NEW YORK COMPUTER: EIBM PC COMP COMPUTER: EIBM PC COMP COMPUTER: EIBM PC COMP COMPUTER: STEMP
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77777777777777777777777777777777777777	RESULT 1 5378464-1 ; Patent No. 5378464 APPLICANT: WOEDER P. TITLE OF INVENTION: MODILATION OF INFLAMMATORY; BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140; NUMBER OF SEDGENCES: 32 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/320,408 FILING DATE: 08-MAR-1989 ;SEQ ID NO:1: LENGTH: 2989	Query Match Best Local S Matches 45 7 2645 CCCC	RESULT 2 US-08-663-566A-1 Sequence 1, Application US/08663566A Patent No. 583733 GENERAL INFORMATION: APPLICANT: Cochran, Mark D APPLICANT: Macdonald, Richard D TITLE OF INVENTION: Recombinant TITLE OF INVENTION: and Uses The NUMBER OF SUGUENCES: 56 CORRESPONDENCE ADDRESS: ADDRESSE: John P. White STREET: 1185 Avenue of the Ame CITY: New York STATE: NEW MORTH REABABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REABABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER REABABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFFWARE: PREFEDIN Release #1. CURRENT APPLICATION NUMBER: US/08/663, FILING DATE: June 13, 1996
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G07947 471 bp DNA STS 05-FEB-1997 human STS CHLC.CTI16.P18204 clone CTI16, sequence tagged site. G07947.1 G1:938497 STS; STS sequence: primer; sequence tagged site. STS; STS sequence: primer; sequence tagged site. STS sequence: primer; sequence tagged site. Human vector-pyCp1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality. Humo saplems.
       Cycles Denaturation Annealing Extension 30 6 60 sec. 60 C 60 sec. 72 C 60 sec. Mg++: 1.50 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34% Albeles: 1.
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1 (Jay.s. 10 471)
Murray, J., Sheffield, V. Weber, J.L., Duyk, G. and Buetow, K. H. Cooperative Human Linkage Center
Dombulished (1995)
Synonyms: CTT16, CHLC. CTT16, #T9987
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75 seconds at 55 degrees C
15 seconds at 72 degrees C
5 minutes at 72 degress C
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Acganism="Homo sapiens"
/Ab xref="taxon:9606"
| map="17"
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| g. 134
| standard_name="STS UTIS4, GDB D175615"
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Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
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each 200 uM
0.3 units
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Thiner B: CCCTTGTTTATTACTTGTTTTCTT
STS size: 174
PCR Profile:
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NH LLABAT STS UTIS4, sequence tagged site.
L29874. GI:821769
STS: PCR PAIMEY: STS sequence; microsatellite DNA; microsatellite
marker; repeat polymorphism; sequence tagged site.
HOMO saplens DNA.
HOMO saplens STS
HOMO saplens STS
BURATOTA: Metacoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukharia: Primates; Catarrhin; Hominidae; Homo.
Eukharia: 1 (Dases I to 370)
GENEN, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
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On May 23, 1995 this sequence version replaced gi:464065.
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corons.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alu-PCR product from mouse/human hybrid cell line 10479 (Coriell Cell Repositories).

Location/Qualifiers
1. 277
Medical Research Council
Addenbrookes Hospital, Hills Road, Cambridge, CB2 20H, England
Fax: 44 (0) 1223 412178
Email: phd@mrc-lmb.cam.ac.uk
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200 uM each
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/db_xref="taxon:9606"
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Primer B: GTACCTCCTTCCTTTCCCTGCT
PCR Profile:
Initial Denaturation: 94C Osec
                                                                                                                   Primer A: GAGTACCTAAGCTTAGTCAGG
Primer B: TCTTAGTCGGGAAAGAGAGG
STS size: 95
Protocol:
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A.thaliana rpl15 gene for plastid ribosomal protein CL15.
211508 1 G1:732561
Tibosomal protein; ribosomal protein CL15.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparalee; Brassicaceae; Arabidopsis. doctyledons; Caparales; Brassicaceae; Arabidopsis. doctyledons; Gast. J.
   Submitted (16-SEP-1993) David A. Fidock, Laboratory of bio-medical parasitology, Pasteur, Institute, 25, rue du Dr. Roux, Paris, PARIS, 7574 CEDEX 15, France
1. Caction/Qualifiers
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Thompson, M.D., Jacks, C.M., Lenvik, T.R. and Gantt, J.S.
Characterization of rps17, rp19 and rpll5: three nucleus-encoded plastid ribosomal protein genes
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lissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
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Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Dimke, D., P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kaymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Veneer, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this ESI, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397871.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Emall: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                    On Dec 3, 1996 this sequence version replaced gi:1119186
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                                                                                                                                                                                                                                                                                                                                    Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850
Fax: 3018699423
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/db_xref="taxon:9606"
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/dev_stage="embryo, 9 wks"
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/organism-"Homo sapiens"
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Contact: Kerlavage, AR
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Sequencing Center
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Columbia University
Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
10032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 259)
Soares, M. B., Bonaldo, M. F., Jelenc, P., Su, L., Lawton, L and Efstratiadis, A. Construction and characterization of a normalized CDNA library Proc. Natl. Acad. Sci. U.S. A. 91, 9228-9232 (1994)
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ph.D., gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sibrary Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Clone distribution: NICARP Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                    seq1091 b4HB3MA Cot8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft287 3', mRNA sequence.
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                                                                                                                                    www-bio.llni.gov/bbrp/image/image.html
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JOURNAL
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AUTHORS
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Direct Submission
Submitted (27-0CT-1998) Microbiology, (
West 12th Ave, Columbus, OH 43210, USA
Location/Qualifiers
                                                                                                                                                                                                                                                  The genes encoding the trimethylamine and dimethylamine methyltransferases of Methanosarcina barkeri are cotranscribed and interrupted by translationally bypassed in frame amber codons Unpublished
                                                                                                                                                                                                                                                                                                                                                     Ferguson, D.J., Gorlatova, N., Paul, L., Grahame, D. and Krzycki, J. The corrinoid protein from Methanosarcina barkeri specific for dimethylamine: Com methyl transfer Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferguson, D. J. Jr. and Krzycki, J.A.
Reconstitution of trimethylamine-dependent coenzyme M methylation with the trimethylamine corrinoid protein and the isozymes of methyltransferase II from Methanosarcina barkeri
J. Bacteriol. 179 (3), 846-852 (1997)
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Paul, L. and Krzycki, J.A.
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/gene="rpl15"
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2678. 2680
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734. .1375
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 function-"participates
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Pred. No. 65;
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5470 ...6873
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/translation-"MAKNANAVAGFNALNGVELNLFTTDELKAIHVATMEVLMDPGIQV
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KVHWTCFGTGVKVCKYQDGKVTVTDSVEKDIADIAKLCDWAENIDYFSLPKSARDIAG
GGAQDYHETLTPLANTAKHSHHIDPVGENVEKJANTGGSSFVYLAGTLVTHNAEVLSGIV
CPTSPLELSVNACQVIIKGARFGIPVNVLSMANSGGSSFVYLAGTLVTHNAEVLSGIV
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AGMMENVERERGKLEFLHYMKAADANTAGVALKDLAPEGASGSKLGVIVNGTVEGD
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SYIELLKEEGLRDKVKVMVGGAPATQAWADKIGADCYAENATEAVAKAKELLA"
SYIELLKEEGLRDKVKVMVGGAPATQAWADKIGADCYAENATEAVAKAKELLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function-"participates in trimethylamine:coenzyme M
methyl transfer with TMA methyltransferase"
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2920. .3573
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KDLATVAHEKVEDVLKNHQVTPIDADIFKDMQAIVDKADKAFRGM*
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/protein_id="AAD14629.1"
/db_xref="GI:4262424"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corrinoid protein"
/codon_start=1
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                                                                                            /translation="MEGYFYDLKALKKOESKRKISKGYMWAFFCAIFWGIWYLPGTYVWTYNTANLAWMYMAFYCAIFWGIWYLPGTYVWYNTPIDEMSSALAKTSGDGISGVYTAYLITAFNALAWMLALMYWMYOVLGKYGELYRT
LKEFHPCSKWFFLASIFGGPWAILGSFIAWGFIGGSFAAVGLLYPYVGSILAYYWYG
EKISKRAAIGIAYIYLGGISIYGGGLFTELSGNVPWIGYLGGLWAAAGWGIEGALAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MANKEEIIAKAKEAITDEDDELAEEV/ANEALAGIDPVELIEKG
FTAGMEEVGEKEGGELELPHVAAAEANNSGIKVITDEMEKKKSQTKSLGTVAIGTI
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NQIQIEEQLKEAGVRDQVKTMVGGAPVTQDWADKIGADIYGESANDAVAKVKAALNV"
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/protein_id="AAD14632.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/product="trimethylamine corrinoid protein MttC"
/protein_id="AAD14631.1"
/db_xref="GI:4262426"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence-experimental
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                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="mttP"
/function="possible methylamine
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                                                             [TFGFCYVTWYKSFPLIGVGRGQGIGNLYGLCAIIFLFLFFGDVPDWTIIIGGALCIA
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3 by N-terminal sequence of corrinoid
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Gaps

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/note=*Organ: liver; vector: pME185-FL3; Site_1: DraIII (CACTGTGTG); site_2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo(dT) primer |

[AIGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sund. Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1 (282 1 to 449)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Ten,F., Underwook,K., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:970652
Seq primer: custom primer used
High quality sequence stop: 448.
                                                                                                                                                                                                                          1 CGTITACAGAITCICTGCGGCTGGCGGTGGAACTACAAAGGGATCGGTGCCTATATCAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ui55c03.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886308 5' similar to TR:014432 014432 TUP1. ;, mRNA
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Contact: Marna Minouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Wouse EST Project
WashIngton University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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                                                                                             Score 63.6; DB 104; Length 596;
Pred. No. 2.2e-05;
0; Mismatches 4; Indels 0;
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/sex="female"
/dev_stage="adult"
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/db_xref="taxon:10090"
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96 9
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                                                                                             23.2%;
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587 AATACCAAAC 596
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Best Local Simi
Matches 66;
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  BASE COUNT
ORIGIN
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AI196903
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="b4HB3MA-COT8-HAP-Ft287"
/clone=lib="b4HB3MA Cot8-HAP-Ft"
/lab_host="E. coli"
/note="Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III;
Size=selected cDNA from polya+ RNA from human brain.
3-month old neonate.This library is the result of an attempted normalization of library b4HB3MA. "
a 50 c 46 g 72 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 596)

2hao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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Pred. No. 1.8e-05;
0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Unpublished (1997)
Conteact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tal: 301 838 0200
Fax: 301 838 0208
     rel: 2129602313
Fax: 2127813577
Email: cuc@cuccfa.ccc.columbia.edu
antisense, Ampicillin
Seg primer: M13 Forward (Universal).
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/db_xref="taxon:9606"
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1. .596
                                                                                                                          Location/Qualifiers
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AQ587717.1 GI:5014397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%;
ilarity 93.9%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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nes 77; Conserv
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human.

ORGANISM

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

RESULT 13 AQ587717 DEFINITION

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source

FEATURES

Query Match

Best Loc Matches

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BASE COUNT

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FEATURES

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822 GGGGTTTCACTGTTAGCCAGGATGGTCTTGATCTCCTGACCT 865

RESULT 14

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Claim 12; Fig 19: 55pp; English.
This sequence represents a human transaldolase (TAL-H) retrotrnspoable element TARE 6. The TAL-H protein can be used in methods to raise antibodies for detecting human transaldolase-mediated neurodegenerative autoimmune diseases, especially multiple sclerosis. The protein has autoimmune diseases, especially multiple sclerosis. The protein has
                                                                       Human polycystic Kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic Kidney disease I semple 5; Pages 60-89; 257pp; English.

C The present sequence is the human polycystic kidney disease I The present sequence is the human polycystic kidney disease I (PKD1) locus between chromosomal markers ATPL (ATP6C) and D16S84.

C The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (AFKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies of ABC be used in diagnostic tests. Anti-PKD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. An are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and to antisense sequences derived from the PKD1 gene may used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Human transaldolase TAL-H TARE-6 retrotransposable element.

Transaldolase; TAL-H; autoantigen; human; antibody; neuroprotector;
neurodegenerative autoimmune disease; multiple scierosis; detection;
proliferation inhibitor; cytotoxicity inhibitor; binding inhibitor;
retrotransposon; retrotrnsposable element; TARE-6; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated human transaldolase gene - useful for raising antibodies for detecting neurodegenerative autoimmune diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                11616
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 53577; 4.3e-10;
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100.0%; Pred. No. 1.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                15782 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3110 GAGACCAGCCTGACCAACATGGTGAAACCCCGTCTCTACTAAAAA 3154
(GENZ ) GENZYME CORP.

Burn T, Connors T, Dackowski W, Germino G, Klinger K,
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100.0%; Pred. No. 4.3
tive 0; Mismatches
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/note= "Alu-sc-like dimer"
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09-APR-1998; US-057762.
(UNNY ) UNIV NEW YORK STATE RES FOUND.
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638. .929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X02711 standard; DNA; 1083 BP
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                                                                                                                                                                                                                                                                                                                                                               nd therapy.
53577 BP;
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09-OCT-1998; 057762.
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WPI; 99-203948/17.
                                      Oian F;
WPI; 98-018511/02.
                                                                                                                                                                                                                                                                                                                                                               detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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The present invention describes hereditary haemochromatosis gene present from the human haemochromatosis gene. The present sequence products from the human haemochromatosis subregion from an hereditary haemochromatosis (HR) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HR) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the bareonce or absence of the haplotype genotype indicates the likely presence of the BRE gene mutation in the genome of the individual. The BRE gene sequences from the present invention can be used to develop protein butyrophilin (BR), and can be used in the production of agonists of invention also describes BRF genes, which are homologues of the milk protein butyrophilin (BR), and can be used in the production of agonists and antagonists of Br function. Also described are: (1) a Roret gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type I sodium transport gene, and can be used for hypophosphetemia.
                                               21-DEC-1998 (first entry)
Hereditary haemochromatosis subregion from an HH affected individual.
Bovine butyrophilin; BT; human hereditary heemochromatosis; HFE;
diagnosis; iron metabolism; NPT3; NPT4; ROREt; BTF1; BTF2; BTF3;
BTF4; BTF5; mik protein; lupus; Sjogren's syndrome; hypophosphatemia;
type 1 sodium transport gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hereditary hamochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e-09;
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100.0%; Pred. No. 1.1e-0;
tive 0; Mismatches
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(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
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062613/C
10 062613 Standard; DNA; 1688 BP.
AC 062613;
DT 17-JAN-1995 (first entry)
DE Human mdr-1 promoter fragment.
KW inducible promoter; cytostatic active cancer therapy; ss.
NG cancer therapy; ss.
PM DE4238778-N.
PD 19-MXY-1994;
PP 12-NOY-1992;
PP 12-NOY-1992;
PP 12-NOY-1992;
PP R 12-N
3/c
V57903 standard; DNA; 237326
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Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1998.
30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-0CT-1996; US-724394.
(PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feder JN, Kronmal GS, La.
Tsuchihashi Z, Wolff RK;
WPI; 98-240014/21.
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Gaps

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Indels

2566 GGGGTTTCACTGTGTTAGCCAGGATGGTCTTGATCTCCTGACCT 2609

Local Similarity 100.0

Matches

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Example 4: Page 440; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain CDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
Intrary as part of a large set of ESTS which can be used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, etc.
Claim 8; page 67-76; 160pp; English.
A human PLAZ-encoding CDNA (081139) expressing HPLAZ-10, was
isolated from human brain RNA by RACE-PCR. 2 Rat PLAZ CDNAS,
designated FNLAZ-8 (Q81136) and RPLAZ-10 (081137), ware isolated from
casignated RPLAZ-8 (Q81136) and RPLAZ-8, respectively. A partial human
genomic counterpart to RPLAZ-8, HPLAZ-8 (Q81139), was also obtained.
RPLAZ-8 and HPLAZ-8 have been designated type III PLAZ, and RPLAZ-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1994 (first entry)
Human brain Expressed Sequence Tag EST02702.
Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Press R63052; R63053.

Novel type III and IV low mol. wt. phospholipase A2 enzymes from humans and rats, also nucleic acid sequences useful, e.g. for recombinant prodn. of enzymes, research into Batten's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3231 TGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCACACCA 3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 43; DB 1; L4
100.0%; Pred. No. 3.2e-09;
iive 0; Mismatches 0;
                         HPLA2-8 gene.
HPLA2-8; phospholipase A2; PLA2; Batten disease;
neuronal ceroid lipfuscinosis; gene therapy; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3789 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1993; U01294.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Adams MD, Moreno RF, Venter CJ;
WPI; 93-272882/34.
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and HPLA2-10 as type IV.
Sequence 15328 BP; 3885 A;
                                                                                                                                                                            /*tag- a //tag- a //tag- a //tag- Exon-1 2633. 2777 /*tag- Exon-2 13862. 14028
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ID Offil08 standard; DNA; 223 BP.

Offil08 and First entry)

DT 16-MAR-1994 (first entry)

E Human brain Expressed Sequence

WW Gene transcription product; gene

KW Gene transcription product; gene

Homo sapiens.

HOW9316178-A.

PR 12-FEB-1993; U01294.

PR 13-72882/34.

PR Adams MD, Moreno RF, Venter CJ;

PR MPT; 93-272882/34.

PT Adams MD, Moreno RF, Venter CJ;

PT Enriched Oilgouncleotides and C most human genes reason CC Library as part of a large set

CC Library as part of a large set
                                                                                                                                                                                                                                                                                                                                             /*tag= c
/label= Exon-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1993; US-097354.
(INCY-) INCYTE PHARM INC.
(INDV ) UNIV INDIANA FOUND.
Sellhamer JJ, Tischfileld JA;
WPI; 95-067096/09.
(first entry)
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Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    L5-JUL-1994; U07926.
15-AUG-1995
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Stein U, Walther W;

WPI: 94-168680/21.

The warm alian expression vector useful for gene therapy, comprising the promoter and/or the enhancer of the mdr-1 gene which is susceptible to cytostatic agents.

This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to hetarclogous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-onocegenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mammalian expression vector useful for gene therapy, comprising the promoter and/or the enhancer of the mdr-1 gene which is susceptible to cytostatic agents.

Claim 2: Page 4: 7pp; German.

Claim 2: Page 4: 7pp; German.

Claim 2: Page 4: 7pp; German.

Claim 3: Page 4: 7pp; German.

Claim 2: Page 4: 7pp; German.

Claim 3: Page 4: 7pp; German.

Claim 3: Page 4: 7pp; German.

Inducible by cytostatic agents on as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the herapeutic agents (e.g. anti-oncogenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of cytostatic agents.
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inducible promoter; cytostatic agent; adriamycin; vincristine; multiple drug resistance; mdr-1; mammalian expression vector; cancer therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 43; DB 1; Length 1688;
100.0%; Pred. No. 3.5e-09;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.5e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      311 C;
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                                                                                                                                                                                                                                                                                                                                                                                                   556 A;
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Best Local Similarity 100.
Matches 43; Conservative
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12-NOV-1992; 238778.
12-NOV-1992; DE-238778.
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Best Local Similarity
Matches 43; Conserva
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                                                                                                                                                                                                                                                                                                                                                                    cytostatic agents.
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WPI; 94-168680/21
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Homo sapiens DE4238778-A.

RESULT 16 Q62612/c

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Sequence

RESULT 17 081139

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Gaps

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Length 15328; Indels

3572 T;

4082 G;

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Query Match
Best Local Similarity
Matches 18; Conserv
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HUMVIPHM1
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KEYWORDS
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                                                                                                FEATURES
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                                                                                                                                                                                                                                                         /db_xref="SPTEMBL:015264"
/db_xref="SPTEMBL:015264"
/translation="MSLIRKKGFYKQDVNKTAWELPKTYVSPTHVGSGAYGSVCSAID
KRSGENVATKKLSREPGSEFFARRAFRAFRAFRAFUD.
FYLVMPFMOTDLORIMGMESFESETOYLYVOH.KGLKYTHGAGVHRDLRGGNLAVNE
PCLKILDFGLARHADAEMTGYVVTRWYRAPEVILSWMHYNOTVDIWSVGCIMAEMIT
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All repeats were identified using Repeat
27782. .27861,29276. .29347,29456. .29570,29695. .29742,
30128. .30207,30365. .30473,33347. .33605,34826. .34955,
36255. .35643))
/gene="Sapk4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC007158 204027 bp DNA HTG 26-0CT-1999 Homo sapiens clone hRPK.90_A_1, *** SEQUENCING IN PROGRESS ***, ordered pieces.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pleces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 10; Length 172048; Pred. No. 1.5; 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone hRPK.90\_A\_1
                                                                                                                                                                                                                                                                                                                                                                                           13.9%; Scc.
100.0%; Pre
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
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EFINITION
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCESSION
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KEYWORDS
SOURCE
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ESULT

COMMENT

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histidine-methionine amide; hormone; peptide hormone; vasoactive
intestinal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA (libraries of Lawn and EMBL), clones lambda-VIP-D and
lambda-VIP-4.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Human vasoactive intestinal peptide and histidine-methlonine a peptide hormone (VIP/PHM-27) gene, exon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 270)
Linders., Barkhem,T., Norberg,A., Persson,H., Schalling,M.,
Hokfelt,T. and Magnusson,G
Structure and expression of the gene encoding the vasoactive
intestinal peptide precursor
Proc. Natl. Acad. Sci. U.S.A. 84 (2), 605-609 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and clean copy of sequence [1] kindly provided by S.Linder, 02-MAR-1987
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                                                                                                                                                                                                                                42; Length 204027;
Score 18; DB 9; Length 270;
Pred. No. 6.7;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="VIP/PHM27 mRNA; G00-120-490"
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                                                                                                                                                                                                                              DB 42
1.5;
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g 58 t
                                                                                                                                                                                                                              Score 19; DB 4
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .270 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/map="6q24-q27"
prim_transcript 100 .>270
/gene="VIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                 13.9%; Scc.
100.0%; Pred
0; N
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100.0%; Prev
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67 c 69
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/gene="VIP"
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                                                                                                                                                                                                                            Query Match 13.9
Best Local Similarity 100.
Matches 19; Conservative
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DNA encoding human gastric inhibitory polypeptide precursor -
used as probe for diagnosis of diabetes and for producing
used as probe for diabetes treatment.

Disclosure; p; Bolish.

Disclosure was obtd. from a clone isolated from a cDNA library
C prepared from total RNA extracted from the duodenum of a patient
during panceato-duodenectomy for pancreatic cancer. The sequence
can be used to design probes (see features) for the diagnosis of
C diabetes. It may also be ligated into an expression vector for
prodn. of recombinant GIP. GIP accelerates the gastric secretion
and insulin secretion and can be used to treat diabetes.
C see also N82432 and N82433.

197 C; 191 G; 191 G; 142 T;
                                                                                                                                                                                                                                                                                                                              /label-probe
/note="used to design probe for diabetes diagnosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="used to design probe for diabetes diagnosis"
553. .658
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Recombinant mosquito salivary allergen rAed a 3 cDNA.
Recombinant; mosquito; salivary allergen; rAed a 3; determination; bite sensitivity; epi-cutaneous test; skin test; intradermal test; allergy diagnosis; immunotherapy; desensitisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANW ) SANWA KAGAKU KENKYUSHO.
Takeda J, Imura H, Seino Y, Tanaka K, Takahashi H, Mitani T;
Kurono M, Sawai K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 15; DB 1; Length 713; 100.0%; Pred. No. 31; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="most likely of the two signals"
                                                                                                                                                                                                                                             /*tag= c
/product=processed GIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 12. .773
                                                                  Location/Qualifiers
101. .562
                                                                                                                                                     'note-"Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V15706 standard; cDNA; 863 BP.
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/label=probe
                                                                                                                 /*tag= a
/label=GIP
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12..65
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                                                                                                                                                                                                    *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 88-148897/22.
P-PSDB; P80287.
                                                                                                                                                                               signal_peptide
                                                                                                                                                                                                                                                                                       other_feature
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                             diabetes; ss.
Homo sapiens.
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Best Local S1
Matches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers
cell growth, particularly cancers
cell growth, particularly cancers
cell growth, particularly cancers
This sequence encodes the human heregular-like factor (HLF) of the invention. The HLF is involved in the regulation of cell growth.

Detection of different levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene expression in cells or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving abnormal levels of HLF activity.

Sequence 536 BP; 141 A; 131 C; 125 G; 120 T;
Example: Fig 2A-H: 98pp; English.

A CDNA molecule (T63334) codes for human nucleoprotein interactor

( (NFT-1) (W16327), a host cell protein which interacts with
influenza virus nucleoprotein (NP) and which may be an accessory
to find the protein influenza virus replication. It is the human
considered for influenza virus replication. It is the human
theractive trap selection using leaxa-NP as identified by
interactive trap selection using leaxa-NP as bait and yeast
transformed with a HeLa CDNA library, and by 5'RACE (see also
coned and analysed. The human NSII-1 gene (T63340), which codes
coned and analysed. The human NSII-1 gene (T63340), which codes
coned and analysed The human MSII-1 gene (T63340), which codes
coned and analysed and interacts with influenza virus protein
NSI was similarly identified. The CDNA clones can be used to
that inhibit viral replication.
Chat inhibit viral replication.
Sequence 2940 BP; 826 A; 641 C; 627 G; 846 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Muman heregulin-like factor coding sequence clone HAGFE38R.
Human heregulin-like factor; HLF; cell growth regulator; diagnosis; neural system disorder; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated heregulin-like factor - used to develop products for
                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hijazi MM, King CR, Ruben SM, Young P;
WPI; 99-095327/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC. (GEOU ) UNIV GEORGETOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X36424 standard; DNA; 536 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ACAGAGATTAGACAAA 108
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         766 ACAGAGATTAGACAAA 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 AGGGTCTTGCCCTTT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 AGGGTCTTGCCCTTT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1998; U12403
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ID N8
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Gastrin inhibitory polypeptide precursor; GIP; probe; insulin;

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Gaps

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This is the MAGE-B cluster DNA sequence. The invention provides a novel method for screening for the possibility of a testicular seminoma, non-small cell lung carcinoma, breast cancer, sarcoma, or at least one nucleic acid molecule which hybridises to mRNA corresponding at least one nucleic acid molecule which hybridises to mRNA corresponding to an MAGE-XP gene, and determining hybridises to mRNA corresponding cossible presence of testicular seminoma, non-small cell lung carcinoma melanoma, breast cancer, sarcoma, or leukaemia in the sample. By assaying for the MAGE-B1 gene, both contained within this 4035 base pair MAGE-B cluster DNA sequence, the presence of such cancers in a sample can be determined. The genomic DNA that encodes the MAGE-B2 gene consists of nucleotides 3266-7979 of this MAGE-B1 gene, consists of in 5' to 3' order, nucleotides 31403-31474, 33958-34062, and 38088-39691, nucleotides 31403-31474, 33958-34062, and 38088-39691, nucleotides 3507-35139 and 38088-39691, and a kit to amplify a MAGE-B gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes hereditary haemochromatosis gene preducts from the human haemochromatosis gene. The present sequence products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual maffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HF) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the harmochromatosis (HF) gene mutation in an individual comprising:

(b) NA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype or genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The presence of the HFE gene mutation in the genome of the individual. The products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and sjonghen's syndrome: and (2) NPT3 and NPT4 genes which are homologues of a type I sodium transport gene, and can can be used for hypophosphatemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hereditary haemochromatosis subregion from an unaffected individual.
Bovina butyrophilin: Br. human hereditary haemochromatosis: HFE;
diagnosis: iron metabolism: NPT3: NPT4: RORet: BTF1: BTF2: BTF3:
BTF4: BTF5: milk protein: lupus; Sjogren's syndrome: hypophosphatemia: type 1 sodium transport gene; ss.
WO9814666-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1909 GGGTTCAAGTGATTCTCCTGCCTTAGCCTCCCGAGTAG 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8269 GGGTTCAAGTGATTCTCCTGCCTTAGCCTCCCGAGTAG 8232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 38; DB 1; L
100.0%; Pred. No. 4.8e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V57926 standard; DNA; 235033 BP.
V57926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hereditary haemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-0CT-1996; US-724394.
(PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolism
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The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HF) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence of a haplotype or genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTE genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BTE function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lugus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
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                                                                                                                                                                                                                                                                                                            21-DEC-1998 (first entry)
Hereditary haemochromatosis subregion from an HH affected individual.
Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
type.l sodium transport gene; ss.
  68340 T;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                           Length 235033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 237326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48217 G;
  49441 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ, Tsuchihashi Z, Wolff RK;
                                                                                                                                                        Db 208777 CAACCTCTGCCTCCCGGGTTCAAGTGATTCTCCCTGCCT 208814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 83860 CAACCTCTGCCTCCCGGGTTCAAGTGATTCTCCTGCCT 83897
                                                         Score 38; DB 1; Le
Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1894 CAACCTCTGCCTCCGGGTTCAAGTGATTCTCCTGCCT 1931
                                                                                                                                   1894 CAACCTCTGCCTCCGGGTTCAAGTGATTCTCCTGCCT 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48904 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1;
Pred. No. 3.8e-0
  48466 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q60985;
16-MAR-1994 (first entry)
Human brain Expressed Sequence Tag EST01661.
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e used for hypophosphatemia 237326 BP; 69596 A; 41
                                         0.9%; Scc.
100.0%; Pre/
0; )
68786 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69596 A;
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100.08; Pre-
                                                                                                                                                                                                                                                                       V57903 standard; DNA; 237326 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   060985 standard; DNA; 382 BP.
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                                                                                                38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998.
30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROG-) PROGENTIOR INC
  235033 BP;
                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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  Seguence
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Q60985
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Best Local S
Matches 37
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19-AUG-1993
12-FEB-1993; U01294
12-FEB-1992; US-837195.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                     (USSH) US DEFT REALE...
Adams MD, Moreno RF, Venter
API; 93-272882/34.
WPI; 93-272882/34.
                                                                                                                                                                                                                                                                        exon
                                            exon
                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                         markers for human genes transcribed in-vivo, facilitate tagging
                                                                                                                                                                                                       Galactokinase; human; mutation;
deficiency: ds.
                        intron
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                    Human galactokinase genomic DNA.
                                                                                                                                                                                                                                        V62906 standard; DNA; 7676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                            13-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                   Local Similarity 
nes 37; Conser
                                                                                                                                                                                                                                                                                                    Conservative
         /rtag= i
/number= 4
                                   /number= 3
2052. .2189
/*tag= h
                                                  /*tag=.g
                      /number 4
2190. .2316
                                                                                   /number=
1762. .18
                                                                                                      1303.
                                                                                                                                                   number-
                                                                                                                                                                      /product= "galactokinase"
                                                                     /number=
                                                                            /*tag-
                                                                                               /*tag=
                                                                                                            number-
                                                                                                                   /*tag-
                                                                                                                                number-
                                                                                                                                       /*tag-
                                                                                                                                                           /*tag=
                                                                                                                                                                                         ocation/Qualifiers
                 /*tag=
                                                             .882. .2051
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                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No.
                                                                                                                                                                                                              detection;
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                                                                                                                                                                                                                                                                                                  DB 1; Le
. 0.0002;
ches 0;
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9854313-A2.
03-DEC-1998.
19-DEC-1998.
17-DEC-1997; US-069865.
17-DEC-1997; US-069865.
30-MAY-1997; US-066340.
(UYMC-):UNIV MCGILL.
Bigey.P. Ramchandani S, Szyf M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5830649-A.
03-NOV-1998.
26-MAY-1995; 451778.
26-MAY-1995; US-451778.
(SMIK ) SMITHKLINE BEECHAM CO.
BETGSHR DJ, Stambollan DE;
WPI; 98-609232/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of galactokinase mutations - based on comparison with wild-type gene sequence or altered galactokinase activity Example 1; Column 27-34; 31pp; English.

This sequence encodes a novel human galactokinase. This protein and its encoding nucleic acid can be used in methods allowing the detection, diagnosis and treatment of human galactokinase deficiency.

Sequence 7676 BP; 1446 A; 2324 C; 2096 G; 1810 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
New DNA methyltransferase nucleotide sequences - used particularly to develop antisense oligonucleotides for disgnostic and therapeutic purposes, particularly for inhibiting tumour growth claim 1; Page 38-40; 108pp; English.

"99091-128 represent DNA methyltransferase (DNA MeTase) genomic fragments. The sequences together sequentially produce the full length sequence v99128. The sequences can be used to derive antisense oligonucleotides which inhibit DNA MeTase expression. The antisense oligonucleotides can be used in investigating the role of DNA MeTase in cellular growth. They can be administered at different points in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA methyltransferase genomic fragment.
DNA methyltransferase; DNA McTase; antisense oligonucleotide; human;
cellular growth; tumour growth inhibition; silenced gene activation;
beta thalassemia; sickle cell anemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3243 AACCTCTGCCTCCCGGGTTCAAGTGATTCTCCTGCCT 3279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                               99-059833/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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6757. .6827
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6995. .7076
/*tag= 0
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7077. .7148
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/*tag= n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7676;
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JOURNAL
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AUTHORS
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
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Submitted (02-OCT-1996)
Submitted by:
Genome Sequencing Center
Genome Sequencing, Washington University,
St. Louis, MO 63110, USA, and
e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The left clone is LUCA21; the right of this cosmid is at base position Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone reference: Ming-Hui Wei et al, 56,1487-1492,1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 32070)
Bentley, D. and Maggi, L.
The sequence of H. sapiens cosmid LUCA22
Unpublished (1996)
2 (bases 1 to 32070)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE INFORMATION: This clone is from a chromosome 3 specific library, VECTOR: pWE15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="ALU" (1876. .2168) /rpt_family="ALU" (1972. .10417) /rpt_family="ALU" (1972. .10417) /rpt_family="ALU" (1974. .10603 ) /rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organisme"Homo sapins"
/db_xef="taxon:9606"
/chromosome="3"
/clone="LUCA22"
/clone="LUCA22"
/clone=11b="LLNL3"
/map="3p21.3"
Complement(join(11435...11560,12513...12642,12721...12818, 13912...13986,14285...14664,15641...1572,15793...15942, 16348...16509,19112...19200.19419...19503.20194...0279, 21578...21650,21735...21812,22312...22399,23017...23114, 24169...24329.24736...24801,25570...25630,26712...26795, 29269...29342,29823...29883))
/note="H_LUCA22.1; coded for by human cDNAs U23946,
                                                                                                                                                                                                                                                                                                          /rpt_family="ALU"
complement(10601.
/rpt_family="ALU"
                                                                                                                                                                                                                                               complement(11435. .29883)
/gene="LUCA15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="ALU"
complement(1876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"ALU" 728. .1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                            .10786)
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1 of HUMLUCA22.
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//Pt_family="ALU"
complement(14318. .14464)
/gene="LUCA15"
/note="Grail prediction, score = 88
complement(14715. .15245)
//Pt_family="ALU"
complement(15002. .15712)
/gene="LUCA15"
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/rpt_family="ALU"
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27411..27822
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23353. .2:
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18664. .18
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/rpt_family="ALU"
                                     /note="close match;
AA03758"
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16740. .17031
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16400. .16673
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//DD_xref="GI:1613
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Sequence:

Description U73168 Human AF091263 Home

Word size Searched: Run on:

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Title:
Perfect score:
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Human cosmid LUCA22,
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U73168.1 GI:1613899
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14.1 32575

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41 AF013452
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AF091263 Homo sapi AF103802 Homo sapi U23946 Human putat AC004814 Homo sapi A74788 Sequence 48 A77777 Sequence 48 A77777 Sequence 3 A69699 Sarcophaga M77345 Rat L-type AC013452 Homo sapi A69681 Sequence 3 A69681 Sequence 3 A69681 Sequence 3 A69681 Sequence 3 AC016250 Homo sapi AC016250 Homo sapi AC017106 Homo sapi AC017106 Homo sapi AC017106 Homo sapi AC011280 Homo sapi AC011280 Homo sapi AC011280 Homo sapi AC012161 Homo sapi AC012161 Homo sapi AC01231 Homo sapi AC013321 Homo sapi AC013321 Homo sapi AC01331 Homo sapi AC013540 Homo sapi AC013540 Homo sapi AC013540 Homo sapi AC018693 Homo sapi AC018691 Homo sapi

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0; Mismatches
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/note="close match;
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/gene="LUCA15"
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/rpt_family="ALU"
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Elst,A., van der Veen,A.Y., Kok,K., Naylor,S.L. and Buys,C.H.C.M.,
An evolutionary rearrangement of the Xpll.3-11.23 region in 3p21.3,
a region frequently deleted in a variety of cancers
Genomics 60 (2), 238-240 (1999)
                                                                                                                                                                                                                                                                                                                                                                                      AF091263 3135 bp mRNA PRI 06-OCT-1999
Homo sapiens RNA binding motif protein 5 (RBM5) mRNA, complete cds.
AF091263
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Elst,A., Voutsinas,M., Hulsbeek,M.M.F., Draaijers,T.G.,
Looman,M.W.G., Kok,K., Naylor,S.L. and Buys,C.H.C.M.
A comparison of genomic structures and expression patterns of two
closely related flanking genes in a critical lung cancer region at
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(Industry 1315)

(Industry 1. Terpstra, P., van den Berg, A., Veldhuis, P.M.J.F., Ter

Elst, A., Voutsinas, M., Hulsbeek, M.M.F., Draaijers, T.G.,

Looman, M.W.G., Kok, K., Naylor, S.L. and Buys, C.H.C.M.

Direct Submission

Submitted (13-SEP-1998) Medical Genetics, University Groningen,

A.Deusinglaan 4, Groningen 9713AW, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3135)
                                                                                                          GGGACTCACTGGTAGTTTGGAGTCTCCCAGCACACCTCCTAGTGGGATGATCTATT
                                           GTTTAGAGGGGTTAGACTCCTTTTTAAAATCTGGATATCTAACCACCTACTTAAATCTGT
                                                                                                                                                                                                                                         CAGCTTTTTCTCTCCTGGCCAGACATGCAGTCTTGCCTTTAGATATCGCAGAGACAAAAT
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/protein_id="AAD04159.1"
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/db_xref="taxon:9606"
/chromosome="3"
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/gene="RBM5"
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QKKLVIQGKHIAMHYSNPRPKFEDMLCNKCCLNNFRKRLKCFRCGADKFDSEQEVPPG
TTESVQSVDYYCDTIILRNIAPHTVVDSIMTALSPYASLAVNNIRLIKDKQTQQNRGF
AFVQLSSAMDASQLLQILQSLHPPLKIDGKTIGVDFAKSARKDLVLSDGNRVSAFSVA
                                                         STATAAAQWSSTQSQSGEGGSVDYSYLOPGODGYAQYAQYSODYQOFYQOQAGGLESD
SSASGATATTTSAAVYSQSPOLYNOTSNPPCQSPTEEAQPSTGSTQAPAASPTGVVP
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AESSSHQOSGLPPAKEGKEKKEKPKRTAQQIAKDMEWAAKSLWKQKENFKNSPOPVN
                                                                                                                                           SLREEERRESAAADAGFALFEKKGALAERÕOLIPELVRNGDEENPLKRGLVAAYSGDS
DNEEELVERLESEERKLADKKKAACLCKROPFNKDALVRNGOLSDLHKONDDIYRRS
RLSEQELEALELREEKK VDRAABREKEKOGIPEPPEPKRKKGPDAGTVVY EOPTKDG
IDHSNIGNKMLQAMGWREGSGLGRKCOGITAPIEAOVRLKGAGLGAKGSAYGLSGADS
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                                                                                                                                                                                                                                                                                                                               /note="zinc finger (C(x2)C(x10)C(x2)C) motif; DNA binding site"
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/gene="RBM5"
/note="RNA-binding motif; unclassified site"
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2093. 2164
/gene="RBM5"
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/gene="RBM5"
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Matches 518; Conservative
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//db_xref="G1:1244404"
/fb_xref="G1:1244404"
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Eukaryota, Metzoca; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2575)
Bader, S., Latif, F., Duh, F., Wei, M., Kashuba, V., Sekido, Y., Lee, C., Koonin, E., Zabarofsky, F., Klein, G., Minna, J.D., and Lerman, M.
A putative tumor suppressor gene LUCAl5 on 3p21.3 encodes two RNA recognizing motifs and is related to the Drosophila tumor
                                                                                                                                                                                                       361 CGACTATAGGCATGACATCAGTGACGAGGAGGGAAGCAAGACCATCATGCTGCGCGGCCT 420
                                                                                                                                                                                                                                                                                                                                                                                    381 CGACTATAGGCATGACATCAGTGACGAGGGGGGGGGCAAGACCATCATGCTGCGCGGCCT 440
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                   AAGAGTGAGTAGAACAGAGCGTAGTGGAAGATACGGTTCCATCATAGACAGGGATGACCG 180
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complete cds.
                                       TGATGAGCGTGAATCCCGAAGCAGGCGGAGGGACTCAGATTACAAAAGATCTAGTGATGA
                                                                                                                      HSU23946 2575 bp mRNA PRI
Human putative tumor suppressor (LUCA15) mRNA,
U23946
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/cell_type="islet beta-cells"
1. .69
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/clone="LUCA15"
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70. .2517
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/do.xref="G1:6048972"
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/tradslation="MASDKNYSTERSGRYGSIIDRDDRDERESRSRRRDSDYKRSSD
DRRGDRYDDYRDYDSPORERERRNSDRSEDGYHSDGDYGEHDYRHDISDERESKTIML
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QKKLVIGGKHTAMHTSRPRFEEDWLCHRCCLNNFRKRLKCFRCGADKFDSFDGEVPPG
TTESVQSVDYYCDTIILRNIAPHTVVDSIMTALSPYASLAVNNIRLIKDKOTQONGGF
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ASSAGTAVITTSAAVVSQSFQLYNQTSNPFGSPTEEAQPSTSTSTQAPAASPTGVVP
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AESSHQQGGLDPAKEGKEKRKRYKSTAQQLAKDMEWAKSLNKQKENEKNESPYN
SLREEPRRESAADDAGFALFEKAAERQQLIPELYNGDDEDPLAKRGLVAAYSGDS
DNEEELYERLESEEEKADWKKMAACLLCRRQPDNKDALVRHQQLSDLHKQNMDIYRRS
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IDHSNIGNKMLQAMGWREGSGLGRKCQGITAPIEAQVRLKGAGLGAKGSAYGLSGADS
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Direct Submission
Submitted (02-NOV-1998) Hematology/Oncology, UCLA School of
Medicine, 5-535 MRL, 675 Circle Drive South, Los Angeles, CA 90095, USA
                                                                                                                                                                                                                                          Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3094)
Oh.J.J., Grosshans.D.R., Wong, S.G. and Slamon, D.J.
Identification of differentially expressed genes associated with
HER-2/neu overexpression in human breast cancer cells
Nucleic Acids Res. 27 (20), 4008-4017 (1999)
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/note="expression increases in HER-2/neu overexpressing
cells; differentially expressed."
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/organism="Homo sapiens"
/organism="taxon:9606"
/clone="H37"
/cell_line="MCF-7/HEE2"
/cell_type="breast adenocarcinoma"
/note="MCF" cells retrovirally transformed with human
HER-2/ney full-length cDNA"
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Pred. No. 6.9e-248;
); Mismatches 1;
523 GCCTGCGGATGTGAGGCTGATGAAGAGGAAAAAAGAGGTG 560
                                                                                   Home sapiens clone H37 unknown mRNA. AF103802 aF103802.1 G1:6048971 FLI_CONA.
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/product="unknown"
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Best Local Similarity 99.8%;
Matches 517; Conservative
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AFYQLSSAMDASQLLQILQSLHPPLKIDGKTIGVDFAKSARKDLVLSDGNRVSAFSVA
ASSASGTAVTTSAAVSQSPQLKVORTLPPGOSPTEBAQPSYGTYDRAPASPTGVY
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SLEREBRRESAAAAGGALPEKKKARLAKSTAQQLAKDBRWAKSLMKQNETNKNSFYPYN
SLEEDERRESAAAAGGALFEKKGALAERQQLIPELVRNGDFENPLKRGLVARSYSGDS
DNEEELVERLESEEEKLADWKKMACLLCRRQFPNKDALVRHQOLSDLHKQNNDIYRRS
TLSQELEAALELRERBYKRRDRAKARGTGTAAFTROFT
IDHSNIGNKMLQAAGGRESGLGRKCQGITAFIEAQVRLKGAGLGARGSAYGLSGADS
YKDAVRRAMFARFIEME
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QKKLVIQGKHIAMHYSNPRPKFEDWLCNKCCLNNFRKRLKCFRCGADKFDSEQEVPG
TTESVQSVDYYCDTIILRNIAPHTVVDSIMTALSPYASLAVNNIRLIKDKQTQONRGF
                                                                                                                                                                                                                                                                                                                                                98 AGTGGGACAATGGGTTCAGACAAAAGAGTGAGTAGAACAGAGCGTAGTGGAAGATACGGT 157
                                                                                                                                                                                                                                                                                                                                                                                      278 GACAGTCCAGAGAGAGCGTGAAAGAAGGAACAGTGACCGATCCGAAGATGGCTACCAT 337
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1 (bases 1 to 83030)
Waterston, R.H.
The Sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                                                38 TCGGTCTCTCCTTGGGAAAAAAAAAAATTTGAACCTTTTGGAGCTGTGTGCTAAAATCTTC 97
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Homo sapiens clone 3938P1, complete sequence.
AC004814
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Pred. No. 4.6e-199;
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99.68;
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NCE 1 (bases 1 to 132)
LE HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
PLACENTA OR BONE DARROW
JRNAL PATENT. (SB): SIBSON DAVID ROSS (GB)
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                                                                                         Louis,
                                                                                                                                                                                                                   Louis,
E 2 (bases 1 to 83030)

S Waterston, R.H.

Direct Submission

L Submitted (12-Juv-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Loui Mo 63108, USA

E 3 (bases 1 to 83030)

E 3 (bases 1 to 83030)

L Submitted (07-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Loui Mo 63108, USA

On Aug 8, 1999 this sequence version replaced g1:3213183.

I 83030

I 83030
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Best Local Similarity 100.0%; Pred. No. 2.3e-55;
Matches 120; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 5.2e-82;
Conservative 0; Mismatches 0;
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18964 c 18150 g 21748
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Sequence 484 from Patent W09401548.
A74798 1 GI:6064812
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/translation="MAGLPLLSLIDELDRESNPSYYGNDFGLGLSPYLIHRQPOREP
AHNIVGYSLPLSLLGSRLNBHQVARRGGEKKEGRYSSPYGKDGFQVCMDVAQFKPSELNV
RVUDMCIVIEGKHEEREDQHGFIQHRFVRRYVLPKGYDADKVVSTLSSDGVLTVSVPK
FYUDMCIVIEGKHEEREDQHGFIQHRFVRRYVLPKGYDGANGEPQEEKK"
195 c 192 g 308 t 308 k
                 Submitted (15-APR-1999) Entomology, Ohio State University, 1735 Neil Ave, Columbus, OH 42210-1220, USA Sequence update by submitter
On Apr 15, 1999 this sequence version replaced gi:2058736.
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Rattus.
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Rat L-type neutral amino acid transporter mRNA, complete cds.
M77345
M77345.1 GI:205238
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
I (bases 1 to 2305;
Tate,S.S., Yan,N. and Udenfriend,S.
Expression cloning of a Na+-independent neutral amino acid
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/protein_id="AAC63387.1"
/db_xref="G1:2058737"
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/db_xref="taxon:59312"
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Proc. Natl. Acad. Sci. U.S.A. 89, 1-5 (1992)
92107996
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Best Local Similarity 100.0%; Pred. No. 7.2e-15;
Matches 47; Conservative 0; Mismatches 0;
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Rattus norvegicus (strain Wistar) cDNA
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Yocum,G.D., Joplin,K.H. and Denlinger,D.L.
Yocum,G.D., Joplin,K.H. and Denlinger,D.L.
pupel diaptation of a 23 kba small heat shock protein transcript during pupel diaptause in the flesh fly, Sarcophaga, crassipalpis Insect Biochem. Mol. Biol. 28 (9), 677-682 (1998)
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Sibson, D.R. and Hadfield, K.M.
Sibson, D.R. and Hadfield, K.M.
HUMAN NUCLEIC ACID FRAGMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,
PLACENTA OR BONE NARROW AND THEIR USE
PACENT: EP 0587279-A 16-MAR-1994;
MEDICAL RES COUNCIL (GB)
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ATTGATGGTTCTTCGAGGTAGTGTTAACTGAAGTGTTCTTCAGTTTGTCAAGATAATGTT 1
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Proc. Natl. Acad. Sci. U.S.A. 95 (10), 5616-5620 (1998)
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                                                          ö
                                                                                                                                                                                                                                     AC013452 184553 bp DNA HTG 12-NOV-1999
Homo sapiens chromosome 15 clone RP11-325E5 map 15q21.1, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;

Eukaryota: Metazoa: Catarrhini: Hominidae: Homo.

1 (bases 1 to 18453)

Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,

Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,

James, R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.

and Hood,L.

Sequencing of human chromosome 15 D15S146-D15S117region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 184553)
2 (bases 1 to 184553)
8 (bases 2, bors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                            Gaps
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Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www.
Contact: leerowendu.washington.edu
Contact: leerowendu.washington.edu
Contact: leerowendu.washington.edu
Contact: leerowendu.washington.edu
Contact: leerowendu.washington.edu
Contact: leerowendu.washington.edu
Sequencing vector: pUCl8: L08752
Chemistry: Big Dye terminators
Assembly program: Phrap; version 0.990399.
* NOTE: This record contains 192 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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                   Length 2305;
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g of 902 bp in length
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gap of unknown length
1802: contig of 888 bp in length
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of 899 bp in length
                 Query Match 1.7%; Score 47; DB 12; L. Best Local Similarity 100.0%; Pred. No. 7.2e-15; Matches 47; Conservative 0; Mismatches 0;
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COMMENT

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/translation-"MSGHAIDPTHTDTLSIHANPOKDOFGAIVAPIYOTSTFLFDNCD
GGARFGGKRAGYMTRIGNPTNSALESGIAALEHABACAARSGMGAAASWWFLK
AGDHISDDCLYGGTHALFBUGNEGVENDFIDMAVPGNIEKHLKRWTRIVYETPA
NPTLKVIDIEDAVKOARKOKDILVIVONTFASPILTNPLDLGVDIVVHSATKYINGHT
VAGTVGSRADIIAKWYSOGIKDITGAIISPHAMIJIRGTLTLDMRWTRAAENAQK
VAGTVGSRADIIAKWYSOGIKDITGAIISPHAMIJIRGTLTLDMRWTRAAENAQK
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VSLAVGIGGPESLIQHPASWIHAGVPKEERRAAGITDNIIRLSVGCENVQDIIDDLKO
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Campbell, R.S., Coombs,G.H., Mottram,J.C. and Pritchard,D.J.
HOMOCYSTEINE DESULPHURASE FROM THE PROTOZOAN TRICHOMONAS VAGINALIS
Patent: WO 9907872-A 26-FEB-1998;
CAMPBELL ROBERT STEWART (GB)
Location/Qualifiers
                                                                                                                                                                 Trichomonas vaginalis.
Trichomonas vaginalis
Trichomonas vaginalis
Trichomonas vaginalis
Usuraryota: Parabasalidea; Trichomonadida; Trichomonas.

(bases 1 to 1305)
Campbell,R.S., Coombs,G.H., Mottram,J.C. and Pritchard,D.J.
HOMOCYSTEINE DESULPHURASE FROM THE PROTOZOAN TRICHOMONAS VAGINALIS
PATENT: WO 9807872-A 26-FEB-1998;
CAMPBELL ROBERT STEWART (GB)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                  /organism="Trichomonas vaginalis"
/db_xref="taxon:5722"
/cell_line="63"
/clone="MGL2"
16. .1212
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1.7%; Score 46; DB 5; Ls
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 46; Conservative 0; Mismatches 0;
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/codon_start=1
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Sequence 11 from Patent W09807872.
A69681.1 GI:4774294
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id-"CAB42512.1"
                                                                                         A69673 1305 bp DNA
Sequence 3 from Patent W09807872.
A69673 GI:4774286
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                                                          of 873 bp in length f unknown length c 900 bp in length f unknown length g of 1203 bp in length f unknown length g of 973 bp in length
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of 940 bp in
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100.0%; Pred. No. 7e-15;
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Query Match Best Local S Matches 47

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1 (Dases 1 to 382)

Tiranti,V., Savoia,A., Forti,F., D'Apolito,M.F., Centra,M., Rocchi,M. and Zevlani,M.

Focchi,M. and Zevlani,M.

polymerase (h-mtRPOL) by cyberscreening of the Expressed Sequence Tags database
Hum. Mol. Genet. 6 (4), 615-625 (1997)
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Submitted (18-CGT-1996) Molecular Medicine, Children's Hospital
Bambino Gesu-IRCS, Piazza S. Onofrio 4, Rome, RM 00165, Italy
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                HSU75370 3832 bp mRNA PRI 23-MAY-1997
Human mitochondrial RNA polymerase mRNA, nuclear gene encoding
mitochondrial protein, complete cds.
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Tiranti,V., D'Apolito,M.F., Forti,F., Rocchi,M., Savoia,A. and
                                                                                           1.7%; Score 46; DB 11; Length 1651;
100.0%; Pred. No. 2.6e-14;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                     /product="mitochondrial RNA polymerase"
/protein_id="AAB58255.1"
/db_xref="G1:2114396"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
/chromosome="19"
/map="19913.3"
33. .3725
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U75370.1 GI:2114395
                                                                                                  Query Match 1.73
Best Local Similarity 100.
Matches 46; Conservative
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HSU75370
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LPATOCLAGKSVTCHVKHTVBSQDVTVPCPVPSTPPTPSPSECCHPRLSL
HRPALDDLLLGSEBANLTCTLTGLEABASCVTFTWTPSSGKSAVGGPPREDLCGCTSVSVS
VLPCCLARGFSPKDVLTATLTATLSKSGNTFRPEVHLLPPPSEELALNEL
VLTCLARGFSFRDVLVANLOGSGELPREKYLTWASRQEPSGGTTTFAVTSLLRVAAE
DWKKGDFFSCMV443 9 316 t
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/td_xref="C1:4774295"
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OGGARFGERGAFYTRIGHTNSALESKIAKLEHARACAATASGMGAIAASWHTFIX
AGDHLISDDGLYGCTHALFEHQLRKFGVEVDFIDMAVPGNIEKHLKPNTRIVYFETPA
NPTLKYTDIBDAVKQARKQKDILVIVDNTFASPILTNRPLDLGVDIVHSATKYINGHT
DVVAGLVGSRADIIAKVYGGGIKDTTGAIISPHDAMLITRGTLTLDMRVKRAAENAQK
VAEFLHEHKAVKKYYFGLEPOHRGHETAKKOKKMFGSAIAFPYDGLEKAKKYLDNCHY
VSLAYSLGGPESLIQHPASMTHAGVPKEERREAAGLTDNLIRLSVGCENVQDIIDDLKQ
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Zheng, S., Cao, J., Cao, W., Cai, X. and Geng, L.

Zheng, S., Cao, J., Cao, W., Cai, X. and Geng, L.

Submitted (19-WAY-1998) Cancer Institute, Zhejiang Medical
University, 68 Jiefang Road, Hangzhou, Zhejiang 310009, P. R. China
2 hangs 1 to 1651)
Zheng, S., Cao, J., Cao, W., Cai, X. and Geng, L.

Direct Submission
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/db_xxref="taxon:9606"
/note="sequence obtained by subtractive hybridization
between normal mucosa and colorectal cancer tissue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.
AF067420
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Identification and characterization of SNC73, a gene which is
down-regulated in colorectal cancer
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1651)
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Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 46; Conservative 0; Mismatches 0; Indels
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/codon_start=1
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join(1. .2867,3029. .3217,3345. .3597,3724. .3903,3959. .12971)
/gene="lvsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEKLELIESICRCTTSALCGNVINRENFEQQIGYKTFSSCLIMTGVLGTEFSKSVVDF
IFDMYTENINASDQISNOMIINNVESFNVILOIIPHTENKDFRLQITSRINKMABYGR
YNOBALSKLSIPDMILSRPENLSANNDPLOPLILLIJGYYGANCLSGSELRQFYKLL
QPERSPEVLLKILSSMAKSPPTPPYFENLSKIPFGTIRVPTIERANPPTKGYTTHW
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                                                                                                                                                                                                                                                                                                                                         Eukaryota: Dictyostellida; Dictyostellum.
1 (bases 1 to 12971)
Kwak,E., Gerald,N., Larochelle,D.A., Vithalani,K.K., Niswonger,M. and De Lozanne,A.
                                                                                                                                                                                                                                                                                                                                                                                                              LVSA, a protein related to the mouse beige protein, is essential for cytokinesis in Dictyostelium Unpublished
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3959. .12603)
/gene="lvsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-AUG-1998) Cell Biology, Duke University Medical Center, 367 Nanaline Duke Building, Durham, NC 27710, USA Location/Qualifiers
                                        Gaps
                                                                                                                                                                                                 AF088979 12971 bp DNA INV 01-SEP-1999
Dictyostelium discoideum beige protein homolog (lvsA) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="LVSA; affected in the REMI cytokinesis mutant
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1.7%; Score 46; DB 10; Length 3832;
100.0%; Pred. No. 2.6e-14;
Live 0; Mismatches 0; Indels
                                                                                           /organism="Dictyostelium discoideum"
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/protein_id="AAD52096.1"
/db_xref="G1:5814091"
                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum.
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De Lozanne, A.
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                   Similarity 100.46; Conservative
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Submitted (31-AUG-
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   Query Match
Best Local S
Matches 46
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FEATURES

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NWDDQEPWEHGHKVPKFHYGTHYSSAAIVLYYLIKLEFFTGHFLKLGGGRWDQPDRLF
STTEAMASSGGSTGVWHELIPEFYYLDFLVNNNKFNFGTKQGGFPIDDIILPPWA
KGSPQEFIKLHRRALESDYVSEHLHEWIDLIFGYRQOGRADDSLWPYYLIYEGAVN
IDAISDPVERAAIIAQINNFGQTPKQLFDKPHPKRNATLMGLPFYAKALTGNFIKDIG
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NYKTSQIANDQITCCIWSKGPEWLGENVLLTGHRDGKVKVWGLETRLLPDNNNSNNNN
NNNNNNNNATQIPSTNNNKLKFKNVIILRATFSNSQSHSTAITSIFLTNDQQKFYTG
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Homo sapiens chromosome 5 clone CIT-HSPC_349C3, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces.
AC010238
AC010238.1 GI:5882694
HTG; HTGS_PHASE1.
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/gene="lvsA"
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COMMENT

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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo saplens chromosome 15, clone RP11-516P9

Lu Unpublished

2 (bases 1 to 78250)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, M., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Crorrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kantes, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, M., McEwan, P., McEwan, P., Norman, C. H., O'Connor, T., Obneal, P., Peterson, K., Pollara, V., Klley, R., Savery, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Charter, J., Wheeler, J., Whith, J., Lintell, A., and Zody, M., Ander, J., Marker, J., Conney, F., Conney, F., Conney, F., Willey, R., Ander, J., Marker, J., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Conney, T., Conney, F., Conney, F., Conney, F., Conney, F., Conney, F., Willey, R., Marker, M., Conney, T., Conney
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Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Homo sapiens chromosome 15 clone RP11-516P9 map 15, LOW-PASS
SEQUENCE SAMPLING.
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Vakaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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contig of 1207 bp in length
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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7328 c 7041 g 67
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AC016250.1 GI:6466544
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                    2 (bases 1 to 28862)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Ethebria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28862)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                    www.jgi.doe.gov.

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www.jgi.doe.gov.

www.jgi.doe.gov.

www.jgi.doe.gov.

tonsists of 32 contigs. The true order of the pieces

tonsists of 32 contigs. The true order of the pieces

to not known and their order in this sequence record is

a true known and their order in this sequence record is

true of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
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20433: contig of 1047 bp in length
gap of unknown length
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gap of unknown length
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gap of unknown length
9198: contig of 647 bp in length
gap of unknown length
9983: contig of 785 bp in length
gap of unknown length
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gap of unknown length
11548: contig of 862 bp in length
gap of unknown length
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gap of unknown length
13854: contig of 686 bp in length
gap of unknown length
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gap of unknown length
17579: contig of 737 bp in length
gap of unknown length
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gap of unknown length
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unknown length
of 650 bp in length
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gap of unknown length
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of 717 bp in le
unknown length
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of 782 bp in
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 107475)
Waterston, R. H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 107475)
Waterston, R. H.
Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC017106 107475 bp DNA HTG 09-DEC-1999
Homo sapiens clone RP11-565G4, LOW-PASS SEQUENCE SAMPLING.
AC017106
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**NOTE: This record contains 186 individual

**NOTE: This record contains 186 individual

**Sequencing reads that have not been assembled into

**contains Runs of N are used to separate the reads

**and the order in which they appear is completely

**arbitrary. Low-pass sequence sampling is useful for

**identifying clones that may be gene-rich and allows

**overlap relationships among clones to be deduced.

**However, it should not be assumed that this clone

**will be sequenced to completion. In the event that

** the record is updated, the accession number will

** be preserved.
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C (bases 1 to 108064)

So Dote Joint Genome Institute.

Direct Submission

L Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jgi.doe.gov.

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence record is

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Homo sapiens chromosome 5 clone CITB-H1_2149024, *** SEQUENCING IN
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Jurect Submission Cambridgeshire, Bubmisted (30-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, Cabonisted (30-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate contig_ID: 00036 Length: 1729bp Contig_ID: 00004 Length: 1361bp Contig_ID: 00101 Length: 1463bp Contig_ID: 00101 Length: 4463bp Contig_ID: 00136 Length: 9012bp Contig_ID: 00136 Length: 4932bp Contig_ID: 00136 Length: 138bp Contig_ID: 00166 Length: 5642bp Contig_ID: 00186 Length: 5642bp Contig_ID: 00186 Length: 2642bp Contig_ID: 00186 Length: 2642bp Contig_ID: 00186 Length: 2642bp
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 140513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL133259 140513 bp DNA HTG 30-NOV-1999
Homo sapiens chromosome 6 clone RP1-258E1, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                     26434 c 26555 g 38040 t
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/db_xref="taxon:9606"
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1422bp
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124805:
125109:
128610:
131764:
                                   116080:
116384:
120735:
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 99103
108657
1108961
116081
116081
120736
121040
124806
125110
128115
131765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-SEP-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
**NOTE: This is a "working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Homo sapiens clone H_NH0113K19, *** SEQUENCING IN PROGRESS ***, 13
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1 (bases 1 to 132333)
MCCOmbie,W.R.
Human Genomic Sequence
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               Score 46; DB 41; Length 108064;
Pred. No. 2.5e-14;
0; Mismatches 0; Indels 0;
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contig of 18570 bp in length
contig of 18570 bp in length
contig of 17199 bp in length
contig of 17199 bp in length
contig of 174620 bp in length
contig of 14620 bp in length
gap of unknown length
contig of 14093 bp in length
contig of 14093 bp in length
gap of unknown length
contig of 11411 bp in length
geap of unknown length
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Pred. No. 2.5e-14;
O: Mismatches 0; Indels
                                                                                            Query Match 1.7%; Score 46; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 46; Conservative 0; Mismatches
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310000
367220
                   1./°,
100.0%; Pre
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McCombie, W.R.
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hes 46; Conservative
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21686
40256
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AC017014_1/C
WPCOMMENT
                     Query Match
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Homo sapiens
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On Nov 29, 1999 this sequence version replaced gi:6066979.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; BCO n's separate contig_ID: 00226 Length: 1287bp Contig_ID: 00228 Length: 1187bp Contig_ID: 00334 Length: 2830bp Contig_ID: 00334 Length: 5230bp Contig_ID: 00491 Length: 6598bp Contig_ID: 00491 Length: 6598bp Contig_ID: 00491 Length: 5620bp Contig_ID: 01100 Length: 5620bp
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Contig_ID: 00515 Length: 2744bp
contig_ID: 00530 Length: 2552bp
Contig_ID: 00630 Length: 1203bp
Contig_ID: 00641 Length: 1863lbp
Contig_ID: 00661 Length: 4896bp
Contig_ID: 00662 Length: 143bp
Contig_ID: 00669 Length: 1754bp
Contig_ID: 00679 Length: 1162bp
Contig_ID: 00670 Length: 1162bp
Contig_ID: 00870 Length: 1351bp
Contig_ID: 00876 Length: 2319bp
Contig_ID: 00878 Length: 219bp
Contig_ID: 00878 Length: 1811bp
Contig_ID: 00878 Length: 1811bp
Contig_ID: 00878 Length: 1811bp
Contig_ID: 00834 Length: 18149bp
Contig_ID: 0081 Length: 1801bp
* NORE: This is a 'working draft' sequence
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144387)
Pavitt,R.
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24991 c 24342 g 33637 t 24806 others
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/organism="Homo sapiens"
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/chromosome="6"
/clone="RP1-258E1"
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AL121601.3 GI:6478115
HTG: HTGS_PHASE1.
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HSDJ315G1
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CE 2 (bases I to 163195)

SE Waterston. H.

Direct Submission

NI Submitted (13-25P-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

ON NOV 5, 1999 this sequence version replaced gl:5871004.

* NOTE: This is a "working draft, Sequence. It currently

* consists of 2 contigs. The true order of the pieces

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 163195)
Waterston, R.H.
Contig_ID: 01138 Length: 5229bp
Contig_ID: 01398 Length: 9434bp
Contig_ID: 01430 Length: 1563bp
Contig_ID: 01776 Length: 22761bp.
* NOTE: This is a "working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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/organism="Homo sapiens"

/chromosome="x"

/map="q24-25"

/clone="itp="ReCI-1"

/clone=lib="ReCI-1"

/clone=lib="ReCI-1"
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/db_xref="taxon:9606"
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Homo saptens clone NH0509E16, *** SEQUENCING IN PROGRESS ***, 17
unordered pieces.
AC012457 GI:6136429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Submitted (19-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Loui University School of Medicine, 4444 Forest Park Parkway, St. Loui MO 63108, USA

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               AC012067 165284 bp DNA HTG 19-OCT-1999
Homo sapiens clone NH0192N14, *** SEQUENCING IN PROGRESS ***, 4
unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165284)
Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165414)
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51 others
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8545; gap of unknown length
49205: contig of 40660 bp in length
49222: gap of unknown length
99112: contig of 48990 bp in length
99129: gap of unknown length
165284: contig of 66155 bp in length.
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100.0%; Pred. No. 2..
... 0; Mismatches
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29550 c 29161 g 52943 t
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/db xref="taxon:9606"
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HTG; HTGS_PHASE1.
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Waterston, R.H.
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Best Local Similarity 100.0
Matches 46; Conservative
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All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp genome.washington.edu/RM/RepeatMasker.thml.

* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is a rbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence to a second will be updated with the finished sequence will
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                                Gaps
                                                                                                                                                                                                                                                                                  AC011280 163533 bp DNA HTG 05-NOV-1999 Homo sapiens clone 13_K_8, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163533)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone 13_K_8
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100.0%; Pred. No. 2.5e-14;
Live 0; Mismatches 0; Indels 0;
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gap of unknown length
50254: contig of 30173 bp in length
gap of unknown length
163533: contig of 113279 bp in length.
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                                Indels
                                                                                   /clone="13_K 8"
/clone_lib="RPCI-11 Human Male BAC"
53421 a 30093 c 29840 g 50177 t 2 c
Pred. No. 2.5e-14;
; Mismatches 0;
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1. .163533
/organism="Homo sapiens"
/db_xref="taxon:9606"
Best Local Similarity 100.0%; P
Matches 46; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                ACO11280
ACO11280.2 GI:6249712
HTG: HTGS_PHASE1.
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Best Local Similarity 100.
Matches 46; Conservative
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Waterston, R.H.
Submission
Submission
Submitted (08-58P-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 53108, USA
On Oct 29, 1999 this sequence version replaced g1:5923976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This 'working draft' quality sequence may consist of several contigs from automated sequence assembly concatenated together. No attempt has been made to order or orient the contigs relative to one another correctly before concatenating. At each location in the sequence where contigs have been joined, several consecutive Ns may have been inserted.
                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 165445)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The attached annotation was produced using a purely automated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The location of this clone is unknown.

* NoTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                            The sequence of Homo sapiens unknown clone NH0418G17
Unpublished
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/rpt_family="MER4-group"

/rpt_family="MER4-group"

/rpt_family="MER4-group"

2998 . 3497

/rpt_family="MER21-group"

/rpt_family="MER21-group"

/rpt_family="GGAA)n"

5536 . 5885

/rpt_family="MER21-group"
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1. .165445
/organism="Homo sapiens"
/db_xref="taxon:9606"
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rpt_family="Retroviral"
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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                                AC009969.3 GI:6139226
HTG; HTGS_PHASE1; HTGS_DRAFT.
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/rpt_family="L1"
5963. .6266
/rpt_family="Alu"
6267. .6690
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                                                                                                               Homo sapiens
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                                                                                                                                                                                      Louis,
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                                                                            To pases 1 to 165414)
Waterston, R. H.
Direct Submission
Submitted (27-0CT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                         2146: contig of 2196 bp in length 214; gap of unknown length 4460: contig of 2246 bp in length 4478: gap of unknown length 8428: contig of 2347 bp in length 8429: contig of 3347 bp in length 1261; gap of unknown length 12621; gap of unknown length 18021: contig of 5400 bp in length 18021: contig of 4805 bp in length 2844: contig of 4805 bp in length 27028: contig of 4805 bp in length 27046; gap of unknown length 27046; gap of unknown length 27046; gap of unknown length 33961: contig of 8915 bp in length 42011: contig of 8915 bp in length 42029: gap of unknown length 69286: contig of 8861 bp in length 61377: gap of unknown length 61377: gap of unknown length 61377: gap of unknown length 63266: contig of 10451 bp in length 6226: contig of 12892 bp in length 82284: gap of unknown length 82284: gap of unknown length 82284: contig of 12892 bp in length 82284: gap of unknown length 21042: contig of 24290 bp in length 21060: gap of unknown length 21061; gap of unknown length 21062: contig of akayon length 21062: contig of unknown length 21062: contig of at 2992 bp in length 21063: gap of unknown length 21063: gap of unknown length 21063: contig of akayon length 21063: gap of unknown length 21063: g
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2.5e-14;
hes 0; Indels
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41694 c 40305 g 42043 t
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Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
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AC009969/c
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DEFINITION
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JOURNAL
                                   TITLE
JOURNAL
        AUTHORS
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33838. .3406"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1.
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REFERENCE AUTHORS TITLE JOURNAL

AUTHORS

TITLE JOURNAL

COMMENT

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Unpublished

E (bases 1 to 169168)

Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Coke, P., Dewark, C., Domino, M., Donelan, L., Doyle, M., Ferrelra, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollarav, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zinner, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zinner, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC013321 169168 bp DNA HTG 30-NOV-1999
Homo saptens chromosome 2 clone RP11-363G3 map 2, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 168363;
  gap of unknown length
contig of 9150 bp in length
gap of unknown length length
ocontig of 11089 bp in length
gap of unknown length
gap of unknown length
contig of 10715 bp in length
contig of 16786 bp in length
gap of unknown length
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1. 168363
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38170 c 36007 g 46468 t 48 others
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Contact: sequence_submission@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                            1.7%; Score 46; DB 42; I
100.0%; Pred. No. 2.5e-14;
Live 0; Mismatches 0;
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Baltren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone 1-H-12

Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone 1-H-12

Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgaler, B., Brown, A., Castle, A., Colangelo, M., Collymore, A.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgaler, B.,

Baldwin, J., Castle, A., Colangelo, M., Collymore, A.,

Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardf, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Kartatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Connoell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                   L Submitted (20-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

** **This is a 'working draft' sequence. It currently consists of 25 contigs. The sequence record is a not known and their corder of the pieces is not known and their corder in this sequence record is arbitrary. Gaps between the contigs are represented as this record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bioinstear, .....
Direct Submission
Submitted (20-JAN-1997) C.K. Blomstedt, Monash University, Genetics
And Developmental Biology, Wellington Road, Clayton, Melbourne,
Victoria 3168, AUSTRALIA
Location/Qualifiers
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                       Sporobolus stapfianus.
Sporobolus stapfianus
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Sporobolus.
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AF005158.1 GI:3719214
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Kohalmi, S.E., Schorr, P., Nowak, J., Reader, L.J. and Crosby, W.L. Direct Submission
Submitted (22-WAY-1997) Gene Expression Group, NRC Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N
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Kohalmi,S.E., Schorr,P., Nowak,J., Reader,L.J. and Crosby,W.L.
The Product of AGAMOUS Interacts with Select Members of the
MADE BOX Family of Proteins in Arabidopsis thaliana
                                                                                                                                                                                                                   Isolation and characterization of cDNAs associated with the or
of desiccation tolerance in the resurrection grass Sporobolus
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/variety="Gandoger"
/db_xref="taxon:56623"
/tissue_type="leaf"
/clone="pSD.8b"
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/protein_id="CAA71753.1"
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Unpublished
2 (bases 1 to 342)
Blomstedt, C.K.
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gap of unknown length
gap of unknown length
35340: contig of 8896 bp in length
gap of unknown length
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of 10006 bp in length
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44797: contig of 9457 bp in length
gap of unknown length
54146: contig of 9349 bp in length
gap of unknown length
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of 1965 bp in length
unknown length
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gap of unknown length
9378: contig of 1852 bp in length
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gap of unknown length
169168: contig of 39512 bp in
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11
1 28671 c 28866 g
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Query Match

Matches

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31

RESULT 3: SSY10781 LOCUS

BASE COUNT ORIGIN

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FEATURES

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Gaps

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Homo sapiens
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                                                                                                                                                                                                                                              /translation="MAREKIRIKKIDNITARQVTFSKRRGIFKKADELSVLCDADVA
LITFSATGKLEFSSSRMRDILGRYSLHASNINKLMPPPSTHLKLENONLSRLSKEVE
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VDENKRLRDKLETLERAKLITLKEALETESVTINVSSYDSGTPLEDDSDTSLKLGLPS
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharyota: Metazoa; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
Sheridan, J. P., Marsters, S.A., Pitti, R.M., Gurney, A., Skubatch, M., Baldwin, D., Ramakrishnan, L., Gray, C.L., Baker, K., Wood, W.I., Goddard, A.D., Goddowsti, P. and Ashkenazi, A.
Control of TRAIL-induced apoptosis by a family of signaling and
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Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D.,
Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D.,
Godowski,P. and Ashkenazi,A.
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inhibits apoptosis induction by TRAIL/Apo2L"
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Homo sapiens decoy receptor 1 (DCR1) mRNA, complete cds.
AF012536
AF012536.1 GI:2338421
                                                                                                                                                                                                                                                                                                                                                                                               DB 8; Length 1016; 9.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
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                                                                                                                                                                                            /product-"MADS-box Protein"
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                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 45; DB
100.0%; Pred. No. 9.3
tive 0; Mismatches
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Submitted (06-JUL-1997) Molecular C
South San Francisco, CA 94080, USA
Location/Qualifiers
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/organism="Homo sapiens"
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Location/Qualifiers
1. .1016
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                                                                                                                                /gene="AGL24"
96. .758
                                                                                                                                                                 /gene="AGL24"
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/gene="DcR1"
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Lebraryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 3105)

RS Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

Direct Submission

AL Submitted (22-JUN-1999) MIPS, Am Klopferspitz 18a D-82152

Martinsriad, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKF2); sequenced by AGOWA within the CDNA

sequencing consortium of the German Genome Project. This clone is

available at the RZPD in Berlin.

Please context the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

//db_rref="taxon:966"
//db_rref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
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GREDDEETKAARDYREGDAGFGRSSTGEERRPAEDORPAGMLPNKTPRGSNRWSRSF
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VPQLHRVSLS"
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TPAABETMTSPGTPAPAAETTMYTSPGTPAPAAEETMTTSPG
TPAPAAEETMTSPGTPASSHTLSCTIVGIIVLLIVFV"
326 c 298 g 218 t
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Homo sapiens mRNA; cDNA DKF2p434J193 (from clone DKF2p434J193)
ALO80137
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/codon_start=2
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Best Local Similarity 100.0%; Pred. No. 9.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 9.3
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; 
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SIISVLPWKRIVAVSAKKKNSKKVQPNSSYQNNITHLNNENLKKSLSCANLSTFAQPP
PAQPPAPPASQLSGSQTGVSSSVKKAPHPAVSSAGTPKRVIVQASTSELLRCLGEFLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S73375 3582 bp mRNA MAM 28-FEB-1995
p25/p35=Cyclin-dependent kinase 5 activator [cattle, brain, mRNA, 3582_nt].
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1. 3582
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/gene="p25/p35"
/fote="Cyclin-dependent kinase 5 activator, Cdk5
activator, P25/P35"
464. 1387
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/protein_id="AaB31984.1"
/db_xref="G1:685112"
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Cochran,M.D. and Macdonald,R.D.
Recombinant herpesvirus of turkeys and uses thereof
Patent: US 5853733-A 1 29-DEC-1998;
Location/Qualiflers
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                                      AR068182 3350 bp DNA
Sequence 1 from patent US 5853733.
AR068182 GI:6000389
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/db_xref="taxon:9913"
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                                                                                                                                           AF106934 3220 bp mRNA PRI 19-MAY-1999
Homo sapiens vitamin D receptor-interacting protein (DRIP92) mRNA,
complete cds.
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Direct Submission
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S Does Joint Genome Institute.

Direct Submission

Submitted (03-A0G-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jqi.doe.gov.

* NOTE: This is a "working draft' sequence. It currently tonsists of 83 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence "as soon as it is available and the accession number will
   RRCYRLKHLSPTDPVLWLRSVDRSLLLQGWQDQGFITPANVVFLYMLCRDVISSEVGS
DHELQAVLLTCLYLSYSYMGNEISYPLKPFLVBSCKEAFWDRCLSVINLMSSKWLQIN
ADPHYFTQVFSQGEDGEDKKRLLLGLDR"
1113 c 1084 g 691 t
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*** SEQUENCING IN
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1 (bases 1 to 41684)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
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                                                                                        1.7%; Score 45; DB 3; Length 3582; llarity 100.0%; Pred. No. 9.2e-14; Conservative 0; Mismatches 0; Indels
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KEYWORDS
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COMMENT

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

E (bases 1 to 55868)

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Goorge, K.A., Harris, N.E., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Fiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
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Direct Submission

Bubmitted (30-JUL-1999) Drosophila Genome Center, Lawrence Berkeley Submitted (30-JUL-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
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Sequencing of Drosophila melanogaster

Unpublished

(bases 1 to 55868)

(calliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,

Eutenhoff, C., Champe, M., Chavez, C., Chew, M., Cissiolka, L.,

Butenhoff, C., Rarfan, D.E., Galle, K., George, R.A., Harris, N.L.,

Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,

Kim, E., Lee, B., Moshrefil, M., Nixon, K., Pacleb, J.M., Park, S.,

Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Shir, E.,

Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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1.7%; Score 45; DB
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tive 0; Mismatches
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Drosophila melanogaster
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HTG; HTGS_PHASE1.
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Direct Submission

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| /organism="Drosophila melanogaster" |
| / Strain="Drosophila melanogaster" |
| / Strain="T; cn bw sp" |
| / Gb_xref="taxon:7227" |
| / Chromosome="3" |
| / Chromosome="3" |
| / Clone="DS00111 (D456)" |
| / Clone="DS00111 (D456)" |
| / Clone="DS00111 (D456)" |
| 15030 a 10666 c 10851 g 15637 t 3684 others
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Human DNA sequence from clone 419C19 on chromosome 1q31, complete
sequence.
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419C19 is from the library RPCI-3 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111079)
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316 52961: contig of 646 bp in length 1962 53041; gap of unknown length 53594: contig of 653 bp in length 695 53774: gap of unknown length 775 54377: contig of 603 bp in length 378 54457; gap of unknown length 6458 55086: contig of 629 bp in length 687 55166; gap of unknown length 688 55188: contig of 629 bp in length 688; contig of 702 bp in length 1167 55688: contig of 702 bp in length.
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HTG; CpG Island.
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Lubratited (30-NOY-1999) Sanger Centre, Hinxton, Cambridgeshire, Submitted (30-NOY-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk
on Nov 15, 1999 this sequence version replaced gi:6136977.
IMPORTANT: This sequence version replaced gi:6136977.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 01957 Length: 128208bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* This record will be updated with the finished sequence
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128208)
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ive 0; Mismatches
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                                                                                        /clone="CIT978SKB_83D3"
40541 a 24231 c 24261 g 36163
Location/Qualifiers
1. 125260
7. organism="Homo sapiens"
Ab_xref="taxon:9606"
/chromosome="5"
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/db_xref="taxon:9606"
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/clone_lib="RPCI-1"
/map="p21.1-21.3"
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AL079341.14 GI:6434655
HTG; HTGS_PHASE1.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC011414 125260 bp DNA HTG 06-OCT-1999
Homo sapiens chromosome 5 clone CIT978SKB_83D3, *** SEQUENCING IN
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12526),
DOE Joint Genome Institute.
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**Www.lgi.doe.gov.

**NOTE: This is a 'working draft' sequence. It currently

* consists of 11 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
 details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
    Location/Qualifiers
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                                                                                                                                                                                                                                               1.7%; Score 45; DB 11; Length 111079; 100.0%; Pred. No. 9e-14; 0; Mismatches 0; Indels 0;
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unknown length
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unknown length
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unknown length
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unknown length
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                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="q31"
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                                                                                                                               /clone_lib="RPCI-3"
/clone="RP3-419C19"
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DOE Joint Genome Institute.
Direct Submission
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AC011414.1 GI:6013528
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                                     111079
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 41
AC011414/c
                                                                                                                                                                      BASE COUNT
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JOURNAL
REFERENCE
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TITLE
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KEYWORDS
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                     FEATURES
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SOURCE

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Homo sapiens
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Best Local Similarity
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                                                 11695
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DEFINITION
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AC015500/c
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ORIGIN
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Baldwin, D., Barnan, N., Backerly, R., Boguslavkiy, L., Boukhgalter, B.,

Baldwin, J., Barnan, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzidgy, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Herton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehockky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., Maclaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Kiley, R. Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Direct Submission

Submitted (O5-OCT-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Nov 19, 1999 this sequence version replaced gi:6012128.

All repeats were identified using Repeatwasker:

Center, Whitehead Institute/ MIT Center for Genome Center Center whitehead Institute/ MIT Center for Genome Center.

Center, Whitehead Institute/ MIT Center for Genome Research
sapiens clone RP11-2P11, WORKING DRAFT SEQUENCE, 21 unordered
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases I to 145346) Bliren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 157000; agarose-fp
Insert size: 145346; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 2_11

Center clone name: 2_11

Sequencing vector: M13: M77815; 100% of reads Sequencing vector: M13: M77815; 100% of reads Assembly program: Phrap: version 0.960731

Consensus quality: 97751 bases at least Q40

Consensus quality: 131236 bases at least Q40

Consensus quality: 136150 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
Center project Information
Center project name: L2689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1091: contig of 1091 bp in length
gap of unknown length
2456: contig of 1365 bp in length
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gap of unknown 1
contig of 2677 b
gap of unknown 1
                                                                        AC011262.2 GI:6454026
HTG: HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                              Unpublished
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DEFINITION
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Date of Dates I to 156730)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Homo sapiens clone RP11-21G19, WORKING DRAFT SEQUENCE, 10 unordered
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1 (bases 1 to 156730)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens; clone RP11-21G19
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                                       contig of 1126 bp in length gap of unknown length gap of unknown length gap of unknown length length gap of unknown length length of 4184 bp in length gap of unknown length length gap of unknown length
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25901 c 27079 g 45152 t 17 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .145346
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-2P11"
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AC015500.2 GI:6553985
HTG: HTGS_PHASE1; HTGS_DRAFT.
contig
gap of
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                                                                                                                                                                                                                                                                     RESULT
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McGurk, J., Malor, J., McGurk, J., McG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 21_G19

Center clone name: 21_G19

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 137650 bases at least 040

Consensus quality: 150175 bases at least 030

Consensus quality: 154137 bases at least 020

Insert size: 156000; agarose-fp

Insert size: 156730; sum-of-contigs
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Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 20601 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 26686 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length 5723: contig of 4562 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown length
contig of 4402 bp in length
gap of unknown
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13408: contig of 3283 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of unknown length contig of 5740 bp in length
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Location/Qualifiers
1. .156730
//db_xref="Homo sapiens"
//db_xref="taxon:9606"
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gap of unknown
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Length 156730;

DB 45;

Score 45;

Query Match

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Dipublished

Underly, Chases I to 162504)

Barran, B. Linton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barran, B., Linton, L., Nusbaum, C., Lander, E., Allen, J., Brown, A., Castel, A., Carny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGrernan, K., McLaughlin, J., Marquis, N., McEwan, P., McGrernan, K., McLaughlin, J., Mella, M., Morris, W., Morrow, J., Mychalecky, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavilin, B., Peterson, K., Pollara, V., Riley, R., Koberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.

Birect Submission submitted (02-Spr-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                         Homo sapiens chromosome 11 clone 397_P_10 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
hNOTE: This is a 'working draft' sequence. It currently a consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as a runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will
                        Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                Indels
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone 397_P_10
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gap of unknown le
5844: contig of 2342 bg
gap of unknown le
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gap of unknown 1
contig of 3045 b
gap of unknown 1
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gap of unknown 1
contig of 3476 b
gap of unknown 1
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gap of unknown
Pred. No. 9e-
Mismatches
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Ouery Match 1.7%; Score 45; DB 42; Length 162504; Best Local Similarity 100.0%; Pred. No. 9e-14; Matches 45; Conservative 0; Mismatches 0; Indels 0;
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/organism="Homo sapiens"
/db_arsei="taxon:9606"
/chromosome="11"
/map="11"
/clone="1397_p_10"
/clone=11b="RRCI-11 Human Male BAC"
a 29955 c 29241 g 50694 t 945 others
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Search completed: April 6, 2000, 14:55:06 Job time: 27491 sec

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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                        Run on:
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High quality sequence stop: 454. FEATURES 1464 /organism="Homo sapiens"	ORIGIN Query Match Query Match Dest Local Similarity Matches 453; DB 49; Length 464; Best Local Similarity Morches 453; Conservative Oy. 1795 ACTGGGAATTCTGGGTTTGGTATTGGTAACTTGATTAATAATTAAT	OY 1855 GAGAGACAGAGCTATTCTCCATGTACTGGCAAGACCTGATTTCTGAGCTTTAATATGGA 1914	Db 284 TICTIGAGGTAAAAGCATCACATGAACTTGTAAAGGAATTTAAAAATCCTACTTTCATAA 225 Qy 2035 TAAGTTGCATAGGTTTAATAATTTTTAATTATATGGGTTTGAATTGTAATTGGGC 2094	Oy 2155 TITGCATGITCAAGAGCCTITITIGAAAAAAGCTITITIGAATCATCAAGT 2214 104 TITGCATGITCAAGAGCCTITITITITITITITITITITITITITITITITITIT	RESULT 2 A1673047 A16
450 19.8 478 50 AL673047 ANB33874 We60all.x 439 19.3 45 AL338791 AL338791 qt53f04.x 432 19.0 697 46 AL399641 AL338791 qt53f04.x 421 19.0 697 46 AL399641 AL399641 LAD8a09.x 422 18.8 447 30 AA243694 AL377357 tc65f01.x AA243694 zr08608.x A1377357 tc65f01.x AA243694 zr08608.x A1377357 tc65f01.x AA243694 zr08608.x AA243694 zr08608.x AA243694 zr08608.x AA243614 tc72 tc3242.d AA243116 AA243116 AA243116 zr08608.x AA233116 zr08608.x AA233116 zr08608.x AA233116 zr08608.x AA233116 zr08608.x AA233116 zr08608.x AA233116 zr08608.x AA333116 AA34319 Tc58609.x AA354319 tc76608.x AA354319 tc76608.x AA35543 tc76608.x AA35543 tc76608.x AA35543 tc76608.x AA35543 tc76608.x AA35578 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA36796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA356796 tc76608.x AA36796 tc76608.x AA367	1.5 294 30 AA25528 1.5 294 47 A464472 1.4 210 4752369 A1646473 1.4 237 51 A0074326 A1607433 1.4 20 47 A5522365 A1607433 1.4 420 48 A5522765 A1601287 1.4 424 51 A1721672 A1721672 1.4 424 51 A1721672 A1721672 1.4 75 34 AA503384 AA503331	1.4 168 44 AU037642 AU03764 1.4 174 41 C94407 1.4 178 61 AI811150 AI811151 1.4 215 64 AW059084 AW059084 1.4 226 69 AW117010 AW11701 1.4 24 43 AU029417 AU0294 1.4 243 44 AU038878 AW090738	1.4 265 74 AW195999 AW195991.4 269 62 AR872568 AR872568 AR87251.4 272 38 AA749402 AA749404 AA7494 AA749404 AA749404 AA7494 AA7494 AA749404 AA749404 AA749404 AA749404 AA749404	AIGE0113 464 bp mRNA EST 10-MAY-1999 We56902.xl Scares_thymus_NHFTh Homo sapiens cDNA clone MMAGE:21345138 3', mRNA sequence. AIGE0113 AIGE0113.1 GI:4763683 EST. human.	M Homo saptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 44) NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap. NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) On Mar 10, 1998 this sequence version replaced gi:2948801. Confact: Robert Strausberg@nih.gov Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "93 c 153 t
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="Scares_thymus_NHFTh"
/dev_stage="fetal"
/lab_host="PH10B (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo(dr) primer [5' retraccarcitritritritritri 3'], retraccarctraagteggaggggcgcaacgtritritritritri 3'],
                                    Tunor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergfaih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq prime: -40UP from gibco
High quality sequence stop: 463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1870 TCTCCATGTACTGGCAAGACCTGATTTCTGAGCATTTAATATGGATGCCGTGGGAGTACA 1929
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210 TAATAATTTTTAATTATATGGCTTGAGTTTAAATTGTAATAGGCGTAACTAATTTTAACT 151
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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RESULT 3 AW183584/c

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a modified polylinker; Site_1: Not I; Site_2: ECO RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHL1)W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297486-302087, 682632-687239, 726408-72871, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

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                                                                                                                                                     Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae: Homo.

Eutheria; Primates; Catarrhini; Hominidae: Homo.

Entional Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), On Doc 20, 1995 this sequence version replaced gi:1135156.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Demail: Robert Strausberg@nih, gov

Tel: (301) 496-1550

Demail: Robert Strausberg@nih, gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

Location/Qualifiers

Location/Qualifiers

Location-Gariane"
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AW183584 494 bp mRNA EST 18-NC
xj77g10.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2663298 3', mRNA sequence.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2663298"
                                                                     AW183584
AW183584.1 GI:6452098
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                                                                                                                                           human.
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                                                                                                                                                                                                                                                                                     2230 AAAGTGTTTGAAAGCTTTA 2248
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Unpublished (1997)

Contact. Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergénih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1870 TCTCCATGTACTGGCAAGACCTGATTTCTGAGCATTTAATATGGATGCCGTGGGAGTACA 1929
                                                             2115 ATGTGTTCATTCTGGAATAATCCTAAACATATGAATTATGTTTGCATGTTCACTTCCAAG 2174
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 24 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 469.
                          AI338791 493 bp mRNA EST 13-FEB-1999 qt551f04.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1951711 3', mRNA sequence.
AI338791. GI:4075718
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100.0%; Pred. No. 3.7e-180;
Live 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1951711"
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                                                                                                                 2235 GTTTGAAAGCTTTA 2248
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I (ppublished (1997)

On Mar 20, 1998 this sequence version replaced gi:2979819.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                     1990 CATCACATGAACTIGTAAAGGAATTTAAAAATCCTACTTTCATAATAAGTTGCATAGGTT 2049
                                                                                                                                                                                                                                                                                                                                                                                                           2110 CTATAATGTGTTCATTCTGGAATAATCCTAAACATATGAATTATGTTTGCATGTTCACTT 2169
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1930 AAAGTGGAGTGTGGCCTGAGTAATGCATTATGGGTGGTTTACCATTTCTTGAGGTAAAAG 1989
                                                                                                                                                                              262 CATCACATGAACTTGTAAAGGAATTTAAAAATCCTACTTTCATAATAAGTTGCATAGGTT 203
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                                       www-bio.lln1.gov/bbrp/image/image.htm1
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/db_xref="taxon:9606"
/clone="IMAGE:2119576"
/clone_lib="NCI_CGAP_Pr28"
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Seq primer: -400P from Gibco
High quality sequence stop: 339.
Location/Qualifiers
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/ulos_lib=soures_nrb_l_cubc_si
/lab_host="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker: Site_l: Not I: Site_2: Eco R;
a modified plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NGL_GAP_GCBL) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was pcR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729906-731399. Subtraction by Bento
Soares and M. Fetima Bonaldo. "
Soares and M. Fetima Bonaldo. "
100 clones of the same of t
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National Cancer Institute, Cancer Genome Anatomy Project
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Best Local Similarity 100.0%; Pred. No. 8.4e-176;
Matches 429; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:2091577"
/clone_lib="Soares_NFL_T_GBC_S1"
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circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 149 c lif g 236 t 2 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
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                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                      Score 432; DB 46;
Pred. No. 3.5e-177;
0; Mismatches 1;
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EST.
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ilarity 99.7%;
Conservative
                                                                                                                                                                                                                                         al Similarity
602; Conserv
                                                                                                                                      194
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2228 ATAAAGTGTTTGAAAGCTTTA 2248
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AI215447/c
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Corganism="Memo sapiens"

Advaref="GDB: 5562549"

Advaref="GDB: 5562549"

Advaref="GDB: 5562549"

Alone="InAGE: 66852"

Alone="InAGE: 66852"

Alone="InAGE: 66852"

Alone="InAGE: 66852"

Alone="InAGE: 68852"

Alone="InAGE: 68852"

Alone="InAGE: Facat haman melanocyte, fetal heart, and pregnant uterus"

Alab.host="Hill B"

Anote="Crgan: mixed (see below): Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecor RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5.000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 444488-489479."
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AR243694 421 DP MRNA EST 07-MAR-1997
Zr68e08.sl Somres_NhHMPu_Sl Homo sapiens cDNA clone IMAGE:668582
3', MRNA sequence.
AR243694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fred. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1868 ATTCTCCATGTACTGGCAAGACCTGATTTCTGAGCATTTAATATGGATGCCGTGGGAGTA 1927
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1 (bases 1 to 42!)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
On May 9, 1995 this sequence version replaced gi:802693.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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ORIGIN
                  AA243694/C
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JOURNAL
COMMENT
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AUTHORS
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/note="Organ: pooled; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHY, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 360) NCI-CGAP http://www.ncbi.nlm.nih.gov/nclegap. NCI-CGAP http://www.ncbi.nlm.nih.gov/nclegap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1950 TAATGCATTATGGGTGGTTTACCATTTCTTGAGGTAAAAGCATCACATGAACTTGTAAAG 2009
                                                                                                                                                1890 CTGATTTCTGAGCATTTAATATGGATGCCGTGGGAGTACAAAAGTGGAGTGTGGCCTGAG 1949
                                                2108 CTCTATAATGTGTTCATTCTGGAATAATCCTAAACATATGAATTATGTTTGCATGTTCAC 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 TTTAATAATTTTTAATTATGCCTTGAGTTTAAATTGTAATAGGCGTAACTAATTTTAA 144
                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                          AI215447 360 bp mRNA EST 22-OC
qhlle04.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1844382 3', mRNA sequence.
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Local Similarity 100.0%; Pred. No. 2.1e-145;
es 359; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1844382"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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/dev_gates="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Corgan: lung: Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
strand cDNA was primed with a sot I - oligo(dT) primer
for TGTTATATATATTTTTTTTTTTT"
double-stranded cDNA was size selected, lighted to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N89899 437 bp mRNA EST 02-APR-1996 252220(9):1 Soares_fetal_ung_NbHL19W Homo sapiens CDNA clone IMAGE:302800 3' similar to SW:ABL_DROME P00522 TYROSINE-PROTEIN KINASE DASH/ABL ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                      1206 TGCCCCAGTTGTTTCTACTACATGGAAGACCTCATTTTGAAGGGAAATTTCAGCAGCTGC 1265
                                                                                                                                                                                                                                                                                                                                  1266 AGCTCATGAGTAACTGATTTGTAACAAGCCTCCTTTTAAAGTAACCCTACAAAACCACTG 1325
                  1026 TCTGAAAGCAACCTTCTTGCCTAGTGTTCTGATATTGGACAGTAAAATCCACAGACCAAC 1085
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 437)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Klucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                 1086 CTGGAGTTGAAATCTTATAATTTTAAAATATGCTCTAAACATGTTTATGGTTGC
                                                                                                                                                                          Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:693457.
Contact: Wilson Ry
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314, 286 1800
Fax: 314, 286 1810
Email: est@watson.wustl.edu
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/clone="IMAGE:302800"
/clone_lib="Soares_fetal_lung_NbHL19w"
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/organism="Homo sapiens"
/db_xref="GDB:1247732"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: ET primer
High quality sequence stop: 359.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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N89899.1 GI:1443226
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
Mahalras,G.G. Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                  AQ784572 535 bp DNA GSS 03-AUG-1999
HS_3248_A2_D01_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3248 Col=2 Row=G, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
University of Washington
University of Washington
Tel: (206) 616-3618
Fax: (206) 616-3887
Enail: jwallace@u washington.edu
Enail: 3248 row: G column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .535
/organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone="plate=3248 Col=2 Row-G"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
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TAATGCATTATGGGTGGTTTACCATTTCTTGAGGTAAAAGCATCACATGAACTTGTAAAG
                                   2010 GAATTTAAAAATCCTACTTTCATAATAAGTTGCATAGGTTTAATAATTTTTAATTATAAG
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E-Coli DH10B"
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Pred. No. 1.3e-134;
0; Mismatches 1;
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High quality sequence stop: 535.
Location/Qualifiers
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AQ784572.1 GI:5692196
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99.78;
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FEATURES
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the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19W."
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Unpublished (19
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Pred. No. 6.4e-126;
0; Mismatches 0;
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ilarity 99.8%;
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// (clone_lib="Soares_fetal_lung_NDHL19w"
// (clone_lib="Soares_fetal_lung_NDHL19w"
// (av_stage="19 weeks"
// (lab_host="DH10B (ampicillin resistant)"
// (lab_host="lab") / (lab="lab") / (lab") /
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zr68e08.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:668582
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Butheria; Primates; Catarrhin!; Hominidae; Homo.

I (bases I to 208)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Hollman, M., Hultman, M., Kloaba, T., Le, M., Lennon, G.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU Merck EST Project
Unpublished (1995)
On Dec 3, 1996 this sequence version replaced gi:1122614.
Contact: Wilson Rv
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 1.4e-94;
ive 0; Mismatches 0;
                                                                            /organism-"Homo sapiens"
                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:1755974"
Location/Qualifiers
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AA233116
AA233116.1 GI:1856110
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Best Local Similarity 100.
Matches 242; Conservative
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Tunor Gene Index
Onpublished (1997)
On May 9, 1996 this sequence version replaced gi:1132712.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: 10101 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
EmmirtBuck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-GGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW001042 359 bp mRNA EST 08-SEP-1999 wr91h07.XL NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495101 3', manA sequence.
AW001042
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 359) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2098 CTAATTTTAACTCTATAATGTGTTCATTCTGGAATAATCCTAAACATATGAATTATGTTT 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2158 GCATGTTCACTTCCAAGAGCCTTTTTTGAAAAAAAGCTTTTTTTGAATCATCAAGTCTT 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 CIAATITITAACTCIAIAATGIGITCATICIGGAAIAATCCIAAACATAIGAATITI 107
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 166;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 155; DB 29;
Pred. No. 8.8e-57;
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                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Scc. No. v. 100.0%; Pred. No. v. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2495101"
/clone_lib="NCI_CGAP_Kidl1"
/lab_host="DH108"
Tel: 82-053-950-5382
Fax: 82-053-955-5327
Email: usohn@bh.kyungpook.ac.kr
Seq primer: M13 Reverse/SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .359
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Best Local Similarity 100.
Matches 155; Conservative
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AW001042/c
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                                                                                                                                                                                                                                                                                                                                                                                   //note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco FR: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHW, pregrant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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                                                                                                                                                                                Sohn, D.S. Park, C.M. Lee, W.K.Cho, H.J.Ahn, M.Y. Lee, M.Y. Hwang, S.W.Jin
Laboratory of Molecular Biology
Kynngpook National University
                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 AATTIAAATATATGCTAAGTCTTATATATTGTAGATAATACAGTTCGGTGAGCTACAAAT 583
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1 (bases I to 166)

1 (bases I to 166)

1 (bases Jank, D.S. Lee, C.M., Cho, W.K., Ahn, H.J., Lee, M.Y., Human HTCDL1 library CDNAs

1 (bases I to 166)

1 (bases I to 166)

1 (bases I to 166)

2 (bases I to 166)

3 (bases I to 166)

3 (bases I to 166)

4 (bases I to 166)

5 (bases I to 166)

6 (bases I to 166)

6 (bases I to 166)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA190204 166 bp mRNA EST 13-JAN-1997
TH075 HTCDL1 Homo sapiens CDNA 5'/3' similar to Unknown, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 GCATTICTAAAGCCATTGTAGTCCTGTAATGGAAGCATCTAG 625
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Best Local Simi
Matches 162;
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Best Local Similarity 100.(
Matches 119; Conservative
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/note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1333911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryora: Merazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

5 Sohn, U., Park, D.S., Lee, C.M., Cho, W.K., Ahn, H.J., Lee, M.Y., Hwang, M.Y. and Jin, S.W.

6 Unpublished (1994)

7 On Sep 12, 1996 this sequence version replaced gi:1294001.

8 Sohn, D.S. Park, C.M. Lee, W.K. Cho, H.J. Ahn, M.Y. Lee, M.Y. Hwang, S.W. Jin Laboratory of Molecular Biology, Manaboratory of Molecular Biology, Manaporatory of Molecular Biology, Molecular Biology, Molecular Biology, Molecular Biology, Molecular Biology, Molecular Biolog
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/db_xref="taxon:9606"
/db_bost="xi-Blue"
/lab_host="xi-Blue"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
EcoRI; Poly(A)-mRNA from the 2-year old male fetal
thymus, oliqo(df) priming, EcoRI cloning in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 TCGTCAAAGCTGAAATGGACTTTTGTACATAGTGAGGAGCTTGAAACGAGGATTGGGAA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.4%; Score 122; DB 63; Length 359; Best Local Similarity 100.0%; Pred. No. 1.3e-42; Matches 122; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA585096 172 bp mRNA EST 09-,
AA1847 HTCDL1 Homo sapiens CDNA 5'/3', mRNA sequence.
AA585096.1 GI:2384984
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Fax: 82-053-955-5327
Email: usohnébh.kyungpook.ac.kr
Seq primer: MJ Reverse/SK primer.
Location/Qualifiers
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AASB5096
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Score 119; DB 35; Length 172;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dages I to 331)
Adams,M.D., Karlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G. Blake,J.A., Brandon,R.C., Man'Wal.C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Bandewal, E.S.Jr.,
Kelley,J.M., Kalley,J.C., Liul,L.I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Ngudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weddek,D.M., Shirley,R.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Colleman,T.A., Collins,E.J.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Fischer,C., Hastings,G.A.,
Hew,W., Hu,J.S., Greene,J.W., Gruber,J., Hudsen,P.K., Kan,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Coleman,M.R., Raser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
                                    ö
                                                                                                                                                                                                                                                                                                                                AA354319 331 bp mRNA EST 21-APR-1997
EST62569 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence.
AA354319.1 GI:2006639
EST.
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For clone availability, additional sequence and expression
information related to this EST, please check the TiGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                           2099 TAATTTTAACTCTATAATGTGTTCATTCTGGAATAATCCTAAACATATGAATTATGTTTG 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="ATCC (inhost):154561"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                       0; Gaps
                                                                                                                         On May 8, 1995 this sequence version replaced gi:801515.
Other_ESTs: THC148776
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 301869956
Fax: 3018699423
                                Indels
100.0%; Pred. No. 3.6e-41; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.9%; Score 111; DB 32; 100.0%; Pred. No. 8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 t
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality, sequence stop: 216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 CCAAGAGICCACCAGGCCATGGACGCAGTGGCTGTGTATCATGGCAAAATCAGCAGGGAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ACCGGCGAGAAGCTCCTGCTTGCCACTGGGCTGGATGGCAGCTATTTGCTGAGGGACAGC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 CCAAGAGTCCACCAGGCCATGGACGCAGTGGCTGTGTATCATGGCAAAATCAGCAGGGAA 92
                                                                          Vertebrata; Mammalia;
                                                                                                         1 (bases 1 to 477)
Hillier,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M., Rucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Riftin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                 The WashU-Merck EST Project
Unpublished (1995)
Unpublished (1995)
Un Jan 24, 1995 this sequence version replaced gi:634373.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2%; Score 73; DB 26; Length 477; 99.2%; Pred. No. 2.1e-21; .ive 0; Mismatches 1; Indels
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 GI:1295392
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Matches 123; Conservative
                                                      Homo sapiens
   W19453.1
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AA355783
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Email: usohn@bh.kyungpook.ac.kr
Email: usohn@bh.kyungpook.ac.kr
EST is putatively homologous to ATPase 1 (PIR, A44396) in
Flasmodium falciparum with 50% (5 amino acids overlapped) identity.
Seq primer: Mi3 Reverse/5K primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .150
/organism="Homo sapiens"
//db_xef="taxon:9606"
/clone_lib="HTCDLU"
/lab_host="XLI-Blue"
/note="Vector: pBluescript SK(-); Site_l: EcoRI; Site_2:
EcoRI; Poly(A)-mRNA from the 2-year old male fetal
thymus, oligo(JT) priming, EcoRI cloning in the vector
pBluescipt (Stratagene)."
a 23 c 19 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sohn, D. S. Park, C. M. Lee, W. K. Cho, H. J. Ahn, M. Y. Lee, M. Y. Hwang, S. W. Jin Laboratory of Molecular Biology
Kyungpook National University
                                                                                                                                                                                                                                         T25937 150 bp mRNA EST 10-MAR-1998 ATH237 HTCDL1 Homo sapiens cDNA 5'/3' similar to ATPase 1, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2136 CCTAAACATATGAATTATGTTTGCATGTTCACTTCCAAGAGCCTTTTTTTGAAAAAAAGC 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 CCTAAACATATGAATTATGTTTGCATGTTCACTTCCAAGAGCCTTTTTTTGAAAAAAGC 102
                                                        49 CATGGACGCAGTGGCTGTGTATCATGGCAAAATCAGCAGGGAAACCGGCGAGAAGCTCCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                     102 CATGGACGCAGTGGCTGTGTATCATGGCAAAATCAGCAGGAAACCGGCGAGAAGCTCCT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #19453 477 bp mRNA EST 03-MAY-1996 zb2zc09.rl Scarcs_fetal_lung_NbHL19W Homo sapiens CDNA clone WIMAGE:302800 5', mRNA sequence.
   Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sohn,U., Park,D.S., Lee,C.M., Cho,W.K., Ahn,H.J., Lee,M.Y.,
Hwang,M.Y. and Jin,S.W.
Human HTCDL1 library cDNAs
Uppublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Genetic Eng., Kyungpook National Univ., Taegu 702-701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
   ;
                                                                                                             162 GCTTGCCACTGGGCTGGATGGCAGCTATTTGCTGAGGGACAGCGAGAGCGT 212
                                                                                                                               109 GCTTGCCACTGGGCTGGATGGCAGCTATTTGCTGAGGGACAGCGAGAGCGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 Similarity 100.0%; Pred. No. 4.2e-25; Conservative 0; Mismatches 0; Indels
   Indels
   ö
   Mismatches
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rz5937.1 GI:2947531
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   Matches 111; Conservative
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                                                                                                                                                                                                                                                                                  sednence.
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KEYWORDS

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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
71e1: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the CDNA between the NotI site and the
Oligo-dr track served to identify it as a clone from the normalized
adult 8-Day-Embryo library. CDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Gragnism *Ratus noivegicus / Gragnism *Ratus noivegicus / Gragnism *Ratus noivegicus / Gragnism *Ratus noivegicus / Grae="UI-R-CO-itr-a-04-0-UI" / Glone="UI-R-CO-itr-a-04-0-UI" / Glone="UI-R-CO" / Glone="UI-R-A" / Glone="UI-R-CO" / Glone="
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Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 590)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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100.0%; Pred. No. 2e-08;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Rattus norvegicus"
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                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
97044477
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Best Local Similarity 100.0
Matches 43; Conservative
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                                                                                                                                         discovery
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AI131797
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                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Whiteo,S. Blake,J.G., Blake,J.G., Man-Wal,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Genelm,C.L., Hanna,M.C., Hedollom,E., Hinkle,P.B.,J.C., Kelley,J.M., Melley,J.C., Liu,L.T., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.S., Scott,J.L., Saudek,D.M., Gollins,E.J., Li,Y., Bednarik,D.P., Capeda,M.A., Coleman,T.A., Collins,E.J., How,W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hudson,P., Kim,A.K., Raymond,L., Wellyer,J.C., Hudson,P., Kim,A.K., Franer,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

L. Nature 377 (6547 Suppl.), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Apr 14, 1993 this sequence version replaced gi:638038.
Other_ESTs: THC148776
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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/organism="Homo sapiens"
/db_xref="ATCC (inbost):157953"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI030232
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FEATURES

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TITLE

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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. RNA and Eco RI Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (Jases 1 to 294)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI464772 397 bp mRNA EST 09-MAR-1999 m277h04.yl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:719479 5' similar to TR:Q61181 Q61181 INOSITOL POLYPHOSPHATE-5-PHOSPHATASE, 145 KDA ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                  Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:638194, Contact: Marana MyMouse EST Project
Washb-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 397)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse lymph node NbMLN"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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100.0%; Pred. No. 7.8e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 275. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               # CGAGTGTCCCAGACAGAACAGGTTCTTGGAGTGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:719479"
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                                                                                                                                                                                    Waterston, R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

1 (Dases 1 to 271)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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AA255258 AA255258.1 GI:1889847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:911904
Seq primer: -20ml3 rev2 ET from Amersham
High quality sequence stop: 89.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                       Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1407241.
Contact: Marra M/Mouse EST Project
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares mouse mammary gland NDMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 35; DB 42; Length 271; 100.0%; Pred. No. 8e-05; ive 0; Mismatches 0; Indels
    POLYPHOSPHATE 5 PHOSPHATASE SIP-145 ;, mRNA sequence
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                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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/db_xref="taxon:10090"
/clone="IMAGE:1400188"
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                                          AI131797.1 GI:3601813
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Gaps

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Mammalia; Mus.

TITLE JOURNAL COMMENT

FEATURES

AUTHORS

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Email: Zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@qenomesystems.com) and Research Genetics, Huntsville. Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU074326 237 bp mRNA EST 24-JUN-1999
AU074326 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSK377, mRNA sequence.
                 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Washu Zebrafish EST Project 1998 Unpublished (1998) On Mar 10, 1998 this sequence version replaced g1:2949061. Contact: Stephen L. Johnson Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Theising, B., Allen, M., Bowers, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.4%; Score 33; DB 47; Length 210; Best Local Similarity 100.0%; Pred. No. 0.00066; Matches 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .210
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
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Seq primer: T7 ET from Amersham
High quality sequence stop: 187.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
Cyprinoidea; Lo 210.
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
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                                                                                                                                       Unpublished (1999)

On May 7, 1998 this sequence version replaced gi:3121624.

Contact: Marra Mywashu-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Far: 314 286 1800

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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fb22e11.x1 2ebrafish WashU MPIMG EST Danio rerio CDNa 3', mRNA
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100.0%; Pred. No. 6.9e-05
iive 0; Mismatches 0
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Seq primer: -40RP from Gibco
High quality sequence stop: 362.
Location/Qualifiers
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Putative full length read
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Query Match Best Local

Matches

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BASE COUNT ORIGIN

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

AI522369/c

RESULT

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Gaps

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Extraction

Extrac
                                                                                                                                                                                                                                                                                 Jab host—"XL1-blue MRF"

// note="Vector: pSPORT1; Site_1: Not1; Site_2: Sall; 1st
strand cDNR was primed with a Not1: Oligo(dT)15 primer
[5/pGACTACTTCTRGATGCGAGCGCCCCTTTTTTTTTTTTTT];
double-stranded CDNA was ligated to Sal I adaptors (BRL),
digested with Not 1 and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). CDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single CDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
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                                                                                                                                                                                                              /tissue_type="26 somite embryos, adult livers, shield
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                                                                                     /db_xref-"taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
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Cyprinoidea: Cyprinidae: Rasborinae; Danio.

I (bases 1 to 301)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptce,M., Thising,B., Allen,M., Bowers,F., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watherston,R. and Wilson,R., Washu Zebrafish Est Project 1998

Unpublished (1998)

On Mar 10, 1998 this sequence version replaced gi:2949468.

Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Fax: 314, 286, 1810
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Actinopterygii,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="AX4"
/db_xref="taxon:44689"
/clone="SSK377"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
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fb62b03.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA 3', mRNA
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                                                                                                                    Developmental cDNA in Dictyostelium discoideum (1999) (hopbblished (1999)) (nopublished (1999)) (no Jun 22, 1998 this sequence version replaced gi:3246998. Contact: Hideko Urushihara (notatt: Arushuba (notatt: 
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Pred. No. 0.00062;
Eukaryota; Dictyostellida; Dictyostellum.
1 (bases 1 to 237)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: zbrafish@watson.wustl.edu
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AI522765
AI522765.1 GI:4436900
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1 (bases 1 to 424)

2 (lark.w. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, T., Watter, E., Kohn, S., Shin, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Washu Zebrafish EST Project 1998

1. Unpublished (1998)

2. Unpublished (1998)

3. On Mar 10, 1998 this sequence version replaced gi:2947976.

3. Other, ESTS: folgoli Johnson

4.444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                         Stage embryos.

[Abb host="XL1" blue MRF"

[Abb host="XL1" blue MRF"

[Abb host="XL1" blue MRF"

[Abb host="XL1" blue MRF"

[Abd Ard Mas Primed With a Not I - oligo(dT) Is primer

[Abd Ard TradfTCGCAGCGCCCTTTTTTTTTTTT]

[Abd Ard Mas Injated to Sal I adaptors (BRL),

digested with Not I and cloned into the Not I and Sal I

sites of the pSPORTI vector (BRL). Library was constructed

by Matthew Clark (Lehrach lab: ICRF, London and Max Planck

Institut fuer Molekulare Genetik, Berlin). cDNAs for EST

analysis were selected following oligonucleotide

hybridization fingerprinting of arrayed clones from

zebrafish late somitogenesis (26 ss), adult liver or

embryonic shield stage (5.6 h) libraries. Fingerprint

data were used to computationally cluster cDNAs, and a

single cDNA from each cluster was chosen for sequencing.

In some cases multiple members of the same cluster were

sequenced to assess clustering parameters or single clones

were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                            /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI721672 424 bp mRNA EST 10-JUN-1999 fc30g11.x1 Zebrafish WashU MPIMG EST Danio rerio CDNA 3', mRNA
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/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
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                                  www.rspd.de)
Possible reversed clone: polyT not found
Seg primer: T7 ET from Amersham
High quality sequence stop: 408.
Location/Qualifiers
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Matches 33; Conservative
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Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, 5t. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@qenomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dassa I to 553)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washir WI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1833180 553 bp mRNA EST 13-JUL-1999 at655f03.x1 Barstead colon HPLRB7 Homo sapiens DNA clone IMAGE:2376893 3' similar to gb:X61100 NADH-UBLQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (HUMAN); mRNA sequence.
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100.0%; Pred. No. 0.00049;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     1 .424 //organism="Danio rerio" //organism="Danio rerio" //db_xref="taxon:7955" //clone_lib="zebrafish WashU MPIMG EST" /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 t
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                                                                                                                                                                                                           Seq primer: 77 ET from Amersham High quality sequence stop: 423. Location/Qualiflers
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AI833180.1 GI:5455160
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/dry and sapiens"

/db xref="Laxon:9606"
/dlone="lawGE:900285"
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/dab_host="lawGE]
/dab_hos
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucabar., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptce, M., Thetsing, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
Public Soybean EST Project
Unpublished (1999)
On Mar 16, 1998 this sequence version replaced gi:2961824.
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3225 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
line@genomesystems.com web site: www.genomesystems.com
Putative full length read
vector to vector length is 804
High quality sequence stop: 132.
Location/Qualifiers
1. 160
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Mataryota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophyte; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1810
Fax: 314 286 1810
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                  primer: -40ml3 fwd. ET from Amersham
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//dev_stage="adult, age 26"
//d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 75)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
On Dec 20, 1995 this sequence version replaced gi:1134468.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
seq primer: -40UP from Gibco
High quality sequence stop: 220.
Location/Qualifiers
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AA503384 GI:2238351
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Unpublished (1997)
On May 18, 1995 this sequence version replaced gi:811178.
Contact: Robert Strausberg, Ph.D.
Fal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="lxhGE:2376893"
/clone_lib="Barstead colon HPLRB7"
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AI811150.1 GI:5397716
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EST.
       Query Match
Best Local Similarity 100.0%
Matches 32; Conservative
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Best Local Similarity 100.0
Matches 32; Conservative
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Dictyostellum discoideum

Dictyostellum discoideum

Eukaryota; Dictyostelida; Dictyostellum.

E (Bases 1 to 168)

S Morto,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Miltra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development

L DNA Res. 5 (6), 335-340 (1998)

E 99156227

On Jan 19, 1998 this sequence version replaced gi:2284680.
                                                                                                                                   /lab_host="DH10B (Gibco BRL)"
//lab_host="DH10B (Gibco BRL)"
//ncte="Vector: pSPORT! (Life Technologies); Site_1: Not I;
Site_2: Sal I; This cDNA library was constructed from mRNA
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the Life Technologies pSuperScript cDNA library
construction kit. Complementary DNA was synthesized from
mRNA using a poly (dT) sequence with a Not I restriction
site. Sal I linkar adapters were ligated to the
blunt-ended cDNA fragments followed by Not I digestion.
The CDNA fragments were directionally cloned into the Not
I'sal I restriction site of the pSpORTI vector. The
ligated cDNA fragments were transformed into E.coli
ElectroMax DH10B host cells (Gibco BRL). This library was
constructed by Dr. Lila Voktin and Dr. Anu Khanna."
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//organ.sn="hottyostelium discoideum"
/strain="A44"
/db_xref="taxon:44689"
/clone="SSE122"
/clone="ib="Dictyostelium discoideum SS (H.Urushihara)"
/dev=stage="slug"
/dev=stage="slug"
/dev=stage="slug"
/dev=stage="slug"
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1019-733"
/clone_lib="Gm-c1019"
/clsue_type="immature seed coats of greenhouse grown plants"
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University of Tsukuba
3.3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'DictyOstelium discoideum cDNA project in Japan',
Location/Qualifiers
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AU037642.1 GI:3984395
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AU037642
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tw37e08.x1 NCI_CGAP_Ut1 Homo sapiens CDNA clone IMAGE:2261894 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Mar 10, 1998 this sequence version replaced gi:2948846.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 495-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                             C94407 174 bp mRNA EST 15-JUN-1998
C94407 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSK659, mRNA sequence.
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SM Dictyostelium discoideum.

Dictyostelium discoideum

Eukaryota: Dictyosteliida; Dictyostelium.

E I (basea) to 11,

S Yoshino,R., Morio,T. and Tanaka,Y.

Developmental CDNA in Dictyostelium discoideum

L Unpublished (1997)

On Jan 14, 1998 this sequence version replaced gi:1797274.

Contact: Hideko Urushihara

Institute of Biological Sciences
University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan

Email: d402hu@sakura.cc.tsukuba.ac.jp

PROJECT - Dictyostelium discoideum cDNA project in Japan.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178)
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1.4%; Score 32; DB 44; Length 168; 100.0%; Pred. No. 0.002; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0019;
tive 0; Mismatches 0
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**ALSURE_TYPE="TO SOBLICE EMBLYOS, AGULT LIVELS, SHIELD STAGE EMBLYOS, AGULT LIVELS, SHIELD STAGE EMBLYOS, AGULT LIVELS, SHIELD STAGE "XLI-blue MRF"

**ADED-host="XLI-blue MRF"

**ATEARD CDNA was primed with a Not I - oligo(d7)15 primer |

**Exand CDNA was planed with a Not I - oligo(d7)15 primer |

**Exand CDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Wax Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster CDNAs, and a single cDNA from each cluster was chosen for sequencing In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Upublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187518.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@thin.gov
Contact: Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/image/image.html
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AIG85109 GI:4896403
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1 (bases 1 to 217)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                 /tissue_type="26 somite embryos, adult livers, shield
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                                                            1. .215
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
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High quality sequence stop: 174.
Location/Qualifiers
1. .217
Seq primer: T7 ET from Amersham
                              Location/Qualifiers
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100.0%; Pre
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15 (Dasses 1 to 215)
16 (Dasses 1 to 215)
18 (Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Edy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Eddy, S., Hillier, E., Kohn, S., Stein, T., Martin, J., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish Est Project 1998
10 upublished (1998)
11 Mashu Ja, 1998 this sequence version replaced gi:3138053.
12 Contact: Stephen L. Johnson
13 Washington University School of Medicine
1444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
14 134 286 1800
                           Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Mashington University Genome

Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

infogenomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
      ä
   fissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
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/organiam="Homo sapiens"
/organiam="Homo sapiens"
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/clone=lib="NGI_CGAP_Utl"
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Query Match 1.4%
Best Local Similarity 100.0
Matches 32; Conservative
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Oryza sativa
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1 (pases I to 226)

2 (lark.M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy, &J., Hilliar,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptec,M., Theising,B., Allen,M., Bowers,Y., Materston,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washu Zebrafish EST Project 1998

N. Unpublished (1998)

On Jun 5, 1998 this sequence version replaced gi:3189699.

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1800

Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matsouri (web address: www.genomesystems.com) (email contact: info@resgen.com) and Resource.

Info@denomesystems.com) and Research Genetics, Huntsville, Alabana (web address: www.resgen.com) (email contact: info@resgen.com) and Ressource.

Sequencing. Try Fre from Amarcham

Sequencing. Try Fre from Amarcham
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/note-"Organ: pancreas; Vector: pCMV-SPORT6; Site_l: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
11548-013"
a 35 c 45 g 81 t
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Location/Qualifiers
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AW117010
AW117010.1 GI:6083348
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Matches 32; Conserv
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AW117010
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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab: ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU029417 237 bp mRNA EST 19-OCT-1998
AU029417 Rice panicle shorter than 3cm Oryza sativa cDNA clone
B20335_62, mRNA sequence.
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Sasaki,T. and Yamamoto,K.
Sasaki,T. and Yamamoto,K.
Sasaki,T. and Yamamoto,K.
Sasaki, Sasaki
Sasaki Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
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3. 0.0017; Indels
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1.4%; Score 32; DB 43; Length 23
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 32; Conservative 0; Mismatches 0; Indels
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/organism="Oryza sativa"
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Tel: 0298 38-7441
Fax: 0298-38-7468
Emall: tsasaki@abr.affrc.go.jp
PROJECT -'RGP'
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/db_xref="taxon:4530"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eltheria; Primates; Catarrhini; Hominidae; Homo.

Eltheria; Primates; Catarrhini; Hominidae; Homo.

NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NI Opublished (1988)

On Jul 9, 1999 this sequence version replaced gi:5435046.

Contact: Robert Strausberg, Ph.D.

Contact: Nobert Strausber
                                                                                                                                            Dictyostellum discoideum.

Eukaryota; Dictyostellum.

Eukaryota; Dictyostellida; Dictyostellum.

(bases 1 to 243)

Morio,T., Urushhara,H., Salto,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

Milliams,J., Waeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of developmental.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="$lug"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Email: d402hu6sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
Location/Qualifiers
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tive 0; Mismatches 0; Indels
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    discoideum cDNA clone SSL587, mRNA sequence.
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/clone="SSL587"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hideko Urushihara
                                                                        AU038878.1 GI:3985631
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Marra, M.; Hiller, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.; Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU038878 243 bp mRNA EST 29-MAR-1999
AU038878 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
                                                                                                                                                                                                                                             AA571665 243 bp mRNA EST 27-AUG-1997 vm09e04.rl Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:989694 5', mRNA sequence. AA571665 G1:2346594
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On May 9, 1995 this sequence version replaced gi:802596.
Contact: Marra MyMouse EST Project
Washb'HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
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(Organism="Homo sapiens"

(Organism="Homo sapiens"

(Ab_xref="taxon:9606"

(Clone=lib="NoI_CGAP_Brn35"

(Clone=lib="NoI_CGAP_Brn35"

(Aisb_host="DHIOB"

(Anote="Organ: brain: Vector: pcMV-SPORT6; Site_1: SalI;

Site_2: NoII; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.33 Kb. Tumor types include:

meningioma, oligodendroglioma, astrocytoma (grade II),

medulloblastoma, astrocytoma (grade IV). Life Technologies

catalog #: 1154-012"
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/strain="AX4"
/db_xref="taxon:44689"
/clone="851480"
/clone="1b="Dictyostelium discoideum SS (H.Urushihara)"
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Dictyostelium discoideum.

Dictyostelium discoideum

Eukaryota, Dictyosteliida; Dictyostelium.

E I toasea I to 256

S Yoshino,R., Morio,T. and Tanaka,Y.

Developmental CDNA in Dictyostelium discoideum

L Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151596.

Contact: Hideko Urushinara

Institute of Biological Sciences

University of Tsukuba

3-10 Ten-nodai, Tsukuba

Bmail: d402hu@sakura.cc.tsukuba.ac.jp.

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 32; Conservative 0; Mismatches 0; Indels
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ENKATYCHE, MATERIA BENEATORIA BENEATORIA MARMALIA:

EUKLATYCHE, METAZOA; CHOTGATA; CTANIATA; VERTEBERATA; MARMALIA:

EUKLATYCHE, METAZOA; CATAITHIN; HOMINIGAE; HOMO.

I (Dases 1 to 265)

RNI-CGAP http://www.ncbi.nlm.nih,gov/ncicgap.

NAIORAL CANCER INSTITUTE, Cancer Genome Anatomy Project (CGAP),

TUMOR Gene Index

AL ORDULIASHO (1997)

On May 18, 1998 this sequence version replaced gi:3137479.

Contact: Robert Strausbergen, Ph.D.

Tel: (301) 466-1550

Email: Robert_Strausbergenih,gov

Infe Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 265.

//organism="Homo sapiens"

//organism="Homo sapiens"

//organism="Homo sapiens"

//clone="Inhacs:2611576"

//clone=lib="NCI_CGAP_Pan1"

//tssue_type="adenocarcinoma"

//lab_host="DH108"

//note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;

//oct="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;

// sapies="Organ: poncreas; Vector: pCMV-SPORT6; Site_1: Sal1;

// sapies="Organ: pcm, scalenge: pcm, sc
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AW195999 265 bp mRNA EST 29-NOV-1999
x186c05.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2681576 3',
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1 (bases 1 to 269)

NCI-CGAP http://www.ncb1.nlm.nlh.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Gene Index (1997)

On Dec 20, 1995 this sequence version replaced gi:1134419.
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AI872568.1 GI:5546617
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COMMENT
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Search completed: April 6, 2000, 13:17:57
Job time: 21662 sec
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                                                     source
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                          FEATURES
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                Email: Robert_Strausberg@alh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl,gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA749402 272 bp mRNA EST 18-FEB-1998 ny04h08.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270815 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthbria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 272)
NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1877690.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                           1..269
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adenocarcinoma, 3 pooled tumors"
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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 32; Conservative 0; Mismatches 0;
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Seq primer: -40ml3 fwd. ET from Amersham
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Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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High quality sequence stop: 266.
Location/Qualifiers
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AA749402.1 GI:2789360
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36 c
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AA749402/c
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TITLE
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High quality sequence stop: 170.
Location/Qualifiers
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AI007840 EST202291
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Match Length DB ID
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qb_gss10:*

qb_gss11:*

em_gss12:*

qb_gss12:*

qb_gss12:*

qb_gss14:*

qb_gss15:*
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9D_est26:*;
9D_est20:*;
9D_est20:*;
9D_est20:*;
9D_est20:*;
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em_est34:*
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gb_gss1:*
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                                                                                             April 6, 2000, 13:18:09; Search time 6421.81 Seconds (Without alignments) 79:372 Million cell updates/sec
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135
1 TICIGACAAIGAGIAAGAAG......AGGGACIGGACIAAAIAAGC 135
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                            4538634 segs, 1887831982 residues
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                                                                   OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_est11:**
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Gaps

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"Sylvata'), 1998 this sequence version replaced g1:2152861.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of lowa
University
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Ratus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryotota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 364)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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(UI-R-BT0) consists of a mixture of individually tagged
                                                                                      1. .278 // Corganisme Rattus sp. " / Organisme Rattus sp. " / Ab_xref = *Arc (inhost):2016112" // Ab_xref = *Arc (inhost):2016112" // Ab_xref = *Arc (inhost):2016112" // Ab_xref = *Arc (inhost):20118" // Ab_xref = *Arc (inhost):20118" // Ab_xref = *Arc (inhost):20118" // Ab_xref = *Arc (inhost):20118 // Ab_xref = *Arc (inhost):2
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UI-R-BTO-Qi-g-12-0-UI.S1 UI-R-BTO RATTUS NOTVEGICUS CDNA CLONE
AI145820
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                                                                                                                                                                                                                                                                                                                                                            41; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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    .364
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                         Query Match 13.3%; Score 18; DB 4 Best Local Similarity 100.0%; Pred. No. 14; Matches 18; Conservative 0; Mismatches
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97044477
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                                                Seq primer: M13-21,
Location/Qualifiers
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Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
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KEYWORDS
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                                                                                    AQ271832 nbxb0026b

B2645 T24A9TR TAM

AQ072249 HS_3024_B

AA20194 xs17d11.s

H73595 ys11b08.s1

AA767354 nz81e12.s

AA767354 nz81e12.s

AA16457 HS_2205_A

AA262551 zs17d11.r

AA28289 nc38c02.r

AA28289 nc38c02.r

AA28259 nc38c02.r

AA28253 nd46c09.s

AA22173 RPC111-64

AG40549 HS_5054_A

AG40549 um25d12.y

AG477193 CTEB-E1-

AG477193 CTEB-E1-

AG577193 CTEB-E1-

AG577193 CTEB-E1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A0278681 CITELE1
A017444 nbxb0009B
A078191 CIT-HSP-2
A0738602 HS_5381_B
B09381 T2449-Sp6 T
AA052408 mb72h01.r
A1278373 qm63e02.x
AV011313 AV011313
AA570404 nk62g08.s
A1277304 qm67f07.x
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T02730 0077M3 gmbP
C34963 C34963 Yuji
C36512 C36512 Yuji
C51747 C51747 Yuji
C52581 C52581 Yuji
C52912 C52912 Yuji
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EST202291 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBRAV56 3' end, mRNA sequence.
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AV184617 AV184617
AV332351 AV332351
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1. (bases 1 to 278)

Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:1900158
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                      AQ271832
B26945
AQ072249
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AQ738602
B09381
AA052408
AI278373
AV011313
AA570404
AQ663218
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AQ657152
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AV184617
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AW106269
    AI007840.1 GI:3221672
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81
27
    Rattus sp.
Rattus sp.
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RESULT 1 AI007840/c LOCUS

DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL TITLE

COMMENT

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normalized libraries constructed from rat hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. The tag used to identify the source tissue is a string of 3-6 nuclectides present between the NoI site and the oligo-dT track which allows the nitreation of the library of origin of a clone within the mixture. This library was then subtracted using a driver consisting of a mixture of all clones from UI-R-AI, UI-R-ED, UI-R-EI, UI-R-CO, UI-R-CI, UI-R-CI and UI-R-CEP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mscares@blue.weeg.ulowa.edu

The sequence contained an oligo-dT track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
trail. The sequence tag present in the CDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized brain library cDNA Library Preparation: M.B. Soares Lab
Glone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 1-34, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_lost="DH10B (Life Technologies)" with a modified
/note="vector: pT713D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1, 447)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIS48491 447 bp mRNA EST 22-MAR-1999
UI-R-C3-to-a-04-0-UI.sl UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-to-a-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 5, 1998 this sequence version replaced gi:3188189.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 13.3%; Score 18; DB 42; Length 364; Best Local Similarity 100.0%; Pred. No. 13; Matches 18; Conservative 0; Mismatches 0; Indels
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/strain="Sprague-Dawley"
/db_xxef="kaxon:10116"
/clone="UI-R-C3-to-a-04-0-UI"
/clone_lib="UI-R-C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
97044477
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AI548491/C
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kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of CDNAs from which ESTS had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C4, UI-R-C0, UI-R-C3, UI-R-C3, UI-R-C2p, UI-R-C4, UI-R-C4), UI-R-C4, UI-R-C4), UI-R-C4, UI-R-C4), UI-R-C5, UI-R-C5), UI-R-C5, UI-R-C5), uI-R-C5, UI-R-C5), uI-R-C5, UI-R-C5), was constructed as follows: Porsamplified contain of a clone within themixture. The subtracted library (UI-R-C3) was constructed as follows: Porsamplified contain of a clone within themixture. The subtracted library (UI-R-C3) was constructed as follows: Porsamplified been derived was used as a driver in a hyporialization with the UI-R-C2P library in the form of single-stranded circles (subtracted library) was purified by hydroxyapatic column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996).
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EST210154 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBRBB71 3' end, mRNA sequence.
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Rattus sp.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 498)
1 Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT/T3Pac; Site_l: EcoRI;
Site_2: NotI"
120 c 108 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 18; DB 48; Length 447; 100.0%; Pred. No. 12; tive 0; Mismatches 0; Indels
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/organism="Rattus sp."
/db_xref="RatCC (inhost):2023824"
/db_xref="taxon:10118"
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AI100865.1 GI:3705892
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Contact: Lee, NH
ATCC
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
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Best Local Similarity
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Arabidopsis.
1 (bases 1 to 175)
Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
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Arabidopsis Genomic Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chale cress. Arabidopsis thaliana Exabidopsis thaliana Eukaryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
Contact: Wing RA
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 7288
Fax: 864 656 7288
Fax: 864 656 7288
Fight: rying@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 88.
Location/Qualifiers
rce
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                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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B26945
B26945.1 GI:2512911
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Best Local Similarity 100.1
Matches 18; Conservative
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EST210619 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBRBL55 3' end, mRNA sequence.
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1 (bases 1 to 903)
Wing, R.A. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1. (bases 1 to 534)

Lee, N.H., Glodes, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.

Ret Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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1. 534

Action Martus Sp. "

Ab_xref="taxtox (inhost):2029307"

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     13.3%; Score 18; DB 43; Length 498; 100.0%; Pred. No. 12; tive 0; Mismatches 0; Indels
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AI101330.1 GI:3706248
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AQ271832.1 GI:3825147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Index
Unpublished (1998)
Other_ESTs: TC54489
Contact: Lee, NH
                                                                                                                                         247 CAAGGGACTGGACTAAAT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 CAAGGGACTGGACTAAAT 131
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                                                                                                               114 CAAGGGACTGGACTAAAT 131
                                                            18; Conservative
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Oryza sativa
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es 18; Conserv
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//ALLIAGE_NOTE TO THE TOTATO 
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                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 44 c 58 g 111 t
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                                                                                                                                                                                   90; Length 340;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                 12.6%; Score 17; DB : 100.0%; Pred. No. 46; tive 0; Mismatches
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/sex="male"
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Best Local Similarity 100.
Matches 17; Conservative
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AA261914
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1 (bases 1 to 340)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
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/db_xref="taxon:9606"
/clone="plate=3024 Col=1 Row=N"
/clone="lib="CIT Approved Human Genomic Sperm Library D"
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
a 31 c 25 g 59 t
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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High Throughput Sequencing Center
Noiversity of Washington North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Exar: (206) 616-3618
Email: jwallace@u.washington.edu
Unpublished (1997)
Other_GSSs: T24A9TFB
Contact: Steve Rounsley
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: rounsley@tigr.org
                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xraf="taxon:3702"
/clone="12489"
/clone_lib="TAMU"
                                                                                                                                                                                                             Email: rounsley@tigr.org
Seg primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 175.
Location/Qualifiers
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Class: BAC ends
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Best Local Similarity 100.
Matches 17; Conservative
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Gaps

RESULT 10 H73595/c LOCUS DEFINITION

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

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Tumor Gene Index
Ontablished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151279.
On Jan 19, 1998 this sequence version replaced gi:2151279.
Contact: Robert_Strausberg@nih.gov
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NGT-GGAP clone distribution information can be found through the I.M.A.GE. Conscritum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA767354 414 bp mRNA EST 08-FEB-1998 nz81e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301902 3',
                                                                                                                                                                                             Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Mammalia; Eutheria: Primates: Catarrhini: Hominidae: Homo. [ (bases 1 to 414) NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap. NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA126408 427 bp mRNA EST 26-NOV-1996 z186h06.rl Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511547 5', mRNA sequence.
AA126408.1 GI:1686020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1301902"
/clone=lib="NCI_CGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 489 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                AA767354.1 GI:2818369
EST.
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Best Local Similarity 100.
Matches 17; Conservative
                                                                       mRNA sequence.
                                                                                                                                                                               Homo sapiens
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AA126408/c
LOCUS
DEFINITION
AA767354/c
LOCUS
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AUTHORS
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                                                                  H73595 404 bp mRNA EST 31-OCT-1995
ysllb08.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
lMAGE:214455 3' similar to gb:x52075_rna3 LEUKOSIALIN PRECURSOR
(HUMAN);, mRNA sequence.
H73595.1 GI:1046654
                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Mammalia; Eutheria: Primates; Catarrhini, Hominidae; Homo.

1 (bases 1 to 404)

Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M., Merdis, E., Moorris, M., Parsons, J., Prange, C., Rifkin, L., Rohling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevsskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., Materston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 1036
High quality sequence stops: 345
Source: IXAGE Consortium, Linl
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: Promega -21ml3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 8, 1995 this sequence version replaced gi:800497. Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 24; Length 404;
Pred. No. 44;
0; Mismatches 0; Indels
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100.0%; Prev
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Best Local Similarity
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FEATURES

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Gaps

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BASE COUNT ORIGIN

Matches

RESULT 11

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Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 435)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On May 8, 1995 this sequence version replaced gi:801104.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

May 18, 1995 this sequence version replaced gi:801104.

Contact: Robert Strausbergenih.gov

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tel: (301) 496-1550

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tel: (301) 496-1550

Tel: (301) 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA262551 435 bp mRNA EST 13-AUG-1997 zs17dll.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685461 5', mRNA sequence.
AA262551 GI:1897913
                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 429.

Location/Qualifiers

Location/Qualifiers

/ .429

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2205 Col=1 Row=M"
/clone="plate=2205 Col=1 Row=M"
/sex=male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" 3 others
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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100.0%; Pred. No. 43;
ive 0; Mismatches 0; Indels
                                                                                                                                              USA
                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USP
Tel: (206) 516-3861
Fax: (206) 516-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2205 row: M column: 1
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/clone=_ilAAGE:685461"

/clone=_ilb="NOI_CGAP_GCB1"

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/lab_host="DH108"
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Best Local Similarity 100.4
Matches 17; Conservative
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                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 427)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Huttman, M., Kucaba, T., Lacy, M., Le, M., M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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HS_2205_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2205 Col=1 Row=M, genomic survey
                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 277.
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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the UDG-cloning

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241 CAATGAGTAAGAAGAAA 257
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In Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1393543.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergaih, gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGP clone distribution information can be found through the II.M.A.G.E. Consortium/LLNL at:
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//note="Vector: pAWPI0; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dTy17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically determined to be prostatic intraepithelial
neoplasia 2 (PIN3) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA228289 447 bp mRNA EST 21-AUG-1997 nc38c02.rl NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010402 similar to contains Alu repetitive element; contains element PTR5 repetitive element; , mRNA sequence.

AA228289 GI:1849850
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1 (bases 1 to 447)

NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
/dev_stage="45 years old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Pr2"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1010402"
                                                                                                                                                                                                                                                                                                                                                                   72 TCTTGCCCTTTGGTTAT 88
                                                                                                                                                                                                                                                                                                                                             29 TCTTGCCCTTTGGTTAT 45
                                                                                                                                                                                                                                                            Query Match 12.6'
Best Local Similarity 100.
Matches 17; Conservative
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/Lone=TrAAGE:158018"
//clone=Ilb="Soarcs_NFL_T_GBC_S1"
/lab_host="DH108"
//clone=Ilb="Soarcs_NFL_T_GBC_S1"
/lab_host="DH108"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH139W, testis NHT, and B-cell NDI_CGAP_GGEBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools of 5,000 clones made from the same 3 libraries. The pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 72648-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " sobressed M. Fatima Bonaldo. " 121 c 126 g 98 t
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Email: Robert_Strausberg@nih.gov
This clone is available royaltyree through LLNL; contact the
This clone is available royalty for further information.
INSET Length: 1658 Std Error: 0.00
Seq primer: -40013 fwd. Er from Amersham
High quality sequence stop: 148.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 451)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 60 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1900158
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                 Length 447;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                          DB 30;
43;
                                                                                                                                                                                                                                                                                          Query Match 12.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 43; Matches 17; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 483)

RS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher.K., Golden,K.,
Berry,K., Ganger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Buliding
Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
Eutheria: Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 476)

8 NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Inmor Gene Index

Inmor Gene Index

Inmor Gene Index

Inmor Gene Index

Interpretation Interpretation: Interpretation In
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
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RPCIII-64B24 TK RPCI-11 Homo sapiens genomic clone RPCI-11-64B24,
genomic survey sequence.
AQ240973 GI:3668557
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High quality sequence stop: 1.
Location/Qualifiers
1. 476
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/db_xref="12axon:9606"
/clone="IMAGE:816016"
/clone="IMAGE:816016"
/tissue_type="bulk tumor"
/lab_host="DH108"
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AQ240973/c
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/cultivar="TA496"
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/clone="type="fulti pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/dev_stage="mature green (3-5 days price: perice: stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Eukaryota: Viridiplantae: Streptophyta; Eukaryota: Viridiplantae: Spermatophyta; Baptantae: Spermatophyta: Gore eudicots: Asteridae: euasterids I: Solanales; Solanaceae; Solanum; Potatoe; Lycopersicon.
I (bases: I to 468)
Alcala, J. Vrebalov, J. White, R., Matern, A. L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Frasef, C.M., Martin, G.B., Tanksley, S.D. and
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                                                                                              AW221275 468 bp mRNA EST 07-DEC-1999
EST297744 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF13N5, mRNA sequence.
AW221275
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glovannoni, J.
Glopublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948814.
Contact: David Frisch
Clemson University
Glomson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4336
Fax: 864 656 4203
Email: dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 523)

1 (bases 1 to 523)

2 NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

3 NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

3 NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

3 NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

3 NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

4 Unpublished (1997)

5 NM 18, 1998 this sequence version replaced gi:3136494.

5 On May 18, 1998 this sequence version replaced gi:3136494.

5 On May 18, 1998 this sequence version replaced gi:3136494.

5 On May 18, 1998 this sequence version replaced gi:3136494.

5 Contact: Robert_Strausberg@hih.gov

7 Tissue Procurement: Cristopher Moskaluk, M.D., Ph.D., Michael R.

5 Email: Robert_Strausberg@hih.gov

7 Tissue Procurement: Cristopher Moskaluk, M.D., Ph.D., Michael R.

5 Emmert-Buck, M.D., Ph.D.

5 Emmert-Buck, M.D., Ph.D.

5 Emmert-Buck, M.D., Ph.D.

5 Emmert-Buck, M.D., Ph.D.

6 CDNA hibrary Arrayed by: Gree Lenonchologies, Inc.

6 CDNA hibrary Arrayed by: Gree Lenonchologies.

7 Clone distribution: NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Conscritum/LLNL at:

7 Www-bio.llnl:gov/bbrp/image/image.html
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="IMAGE: 2187449"
// Clone="IMAGE: 2187449"
// Clone="IMAGE: 2187449"
// Libsue=_Ilb="NoTI_GGAP_Gas4"
// Libsue=_Ilb="NoTI_GGAP_Gas4"
// Lab_host="DH10B"
// Lab_host="DH10B"
// Lab_host="Organ: stomach; Vector: pCMV-SPORT6; Site=_I: SalI; Site_2: NoTI: Cloned unddirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIG12731 523 bp mRNA EST 21-APR-1999 tpllb09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2187449 similar to gb:X06617 40S RIBOSOMAL PROTEIN SI1 (HUMAN);, mRNA
                                               /note="Vector: pBACe3.6; Genomic sequence of BAC ends 101 c 105 g 128 t 6 others
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                      Query Match 12.6%; Score 17; DB 102; Best Local Similarity 100.0%; Pred. No. 41; Matches 17; Conservative 0; Mismatches 0;
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High quality sequence stop: 67.
Location/Qualifiers
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AI612731.1 GI:4621898
                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                     104 ACAAATAAACCAAGGGA 120
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Matches 17; Conservative
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AI612731/c
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High Throughput Sequencing Center
University of Washington
University of Washington
101 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-5618
Fax: (206) 616-51887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@edping.med.buffalo.edu). Clones may be purchased from
BACRAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 630 row: I column: 11
Seq primer: 77
Class: BAC ends
High quality sequence stop: 484.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 484)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                              Location/Qualifiers
1. 481
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| Location/Capacidate
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(pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.idr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ402549 484 bp DNA GSS 13-MAR-1999 HS_5054_A1_E06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=630 Col=11 Row=I, genomic survey sequence.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/oloxref="taxon:9606"
/clone="plate=630 Col=11 Row=1"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 99; Length 483; 41;
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AQ402549.1 GI:4413461
GSS.
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Best Local Similarity 100.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 TIATCATAGAGCAATAA 68
                                                                                                                                                      Seq primer: T/
Class: BAC ends.
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AQ402549/c
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DEFINITION
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Trypanosoma.

1 (pases 1 to 57)
El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujil, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S.,
Donelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                         Venter J.C.
Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
Class: BAC ends.
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Sheared DNA-12F21.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-12F21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBeloBACI1; Site_1: EcoRI; Site_2: EcoRI; CalRech Human BAC Library D" 136 c 78 g 176 t
                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eucheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 533)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trýpanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 40;
0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
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/note="vector: pBel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.6%; Sox
| Similarity 100.0%; Pi
| 17; Conservative 0;
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AQ657152.1 GI:5164920
AQ277193
AQ277193.1 GI:3903389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 CAATGAGTAAGAAGAAA 413
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Best Local Similarity
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AQ657152/c
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/db_cxref="taxon:10090"
/dlone='lub='Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 14 dpc"
/dev_stage="embryo, 15 tarend cDwa was primed
/deb_host='nHi08"
/deb_nost='nHi08"
/dep_stage='lub nost 10 tarend cDwa was primed
with an oligo(dT) primer [ArgraGcCTTTTTTTTTTTTT];
double-stranded cDwa was ligated to a Dralli adaptor
[TGTTGGCTACTGG], digested and cloned into distinct Dralli
sites of the pMERS-Fi3 vector (5' site CACTGTGTG, 3' site
CACCATGG). Xhol should be used to isolate the cDwa
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumlo Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCGCTCTAGAAGCTGCG and 3' end primer
CGACCTGCAGCTGGAGCAR."
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[Obsess 1 to 528]
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ277193 533 bp DNA GSS 22-NOV-1998 CITBI-E1-2522C17.TF CITBI-E1 HOMO Sapiens genomic clone 2522C17, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.ilnl.gov) for further information.
MGI:1005787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                             AW106269 528 bp mRNA EST 20-OCT-1999 um25d12.yl Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2225591 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1134183.
Contact: Marra M/MashU-NCI Mouse EST project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
Tel: 314 286 1810
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Pred. No. 40;
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AW106269.1 GI:6077005
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house mouse.
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DEFINITION
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Gaps

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Eukaryota: Mentacoa: Chordata: Craniata; Vertebrata; Mammalia;
Eukaryota: Metacoa: Chordata: Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini: Hominidae; Homo.

1 (Dases 1 to 618)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSS: CIPBI-E1-2516B5.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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//cell_type="spern"
//ocll_type="spern"
//ocll_type="s
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="F26010"
/clone="F26010"
/clone=lib="IGF"
/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
produced by Thomas Altmann"
94 c 105 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ278681 618 bp DNA GSS 22-NOV-1998 CITBI-E1-2516B5.TR CITBI-E1 Homo sapiens genomic clone 2516B5, genomic survey sequence.
AQ278681 GI:3904649 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                             81; Length 601;
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/clone_lib="CITBI-E1"
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1. 577

1. 577

(organism="Tryposoma brucei" / strain="Tryposoma brucei" / strain="Tryposoma brucei" / strain="Tryposoma brucei" / strain="Tryposoma condition="Sheared DNA-12F21" / clone="Sheared DNA-12F21" / clone population of Tryposoma brucei (TRED927/4 GUTAL 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (MAKing small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press, 1999)."
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Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
Unpublished (1997)

Unpublished (1997)

Other_GSSs: F26010TRC
Contect: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: rounsleyftigr.org
Seq primer: Mi3-21
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1 (bases 1 to 601)

1 (bases 1 to Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and
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Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@iigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for

distribution through ATCC. Sheared DNA end sequences search page:

http://www.iigr.org/tdb/mdb/tbdb/.

Seg primer: Mi3-Forward

class: shotgun.
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F26010TFB IGF Arabidopsis thaliana genomic clone F26010, genomic
survey sequence.
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Location/Qualifiers
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Arabidopsis thaliana
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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

LOCUS

RESULT 2 AQ157444

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Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

12 (Abases 1 to 764)

13 Admas, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

Unpublished (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

The Institute for Genomic Research

Fax: 301 838 0200

Fax: 301 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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HS_5381_B1_B07_SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=957 Col=13 Row=D, genomic survey sequence.
                                                           A0078191 764 bp DNA GSS 20-AUG-1998 CIT-HSP-2360M3.TR CIT-HSP Homo sapiens genomic clone 2360M3, genomic survey sequence.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/ 100.0%; Pred. No. so.
'... 0; Mismatches
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/db_xref="taxon:9606"
/clone="2360M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .764
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AQ738602,1 GI:5516124
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Best Local Similarity 100.
Matches 17; Conservative
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AQ738602/c
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AQ078191/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Cyrya sativa"
//organism="Cyrya sativa"
//strain="Japonica"
//db.xref="taxon:4530"
//clone="lib="CuGI Rice BAC Library"
//clone="lib="CuGI Rice BAC Library"
//clone="lib="CuGI Rice BAC Library"
//lab.host="E.coli DH10B"
//lab.host="E.coli DH10B"
//note="Vector: pBeloBAC11: Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the world. HindIII; Rice as one of two most popular grains in the world. HindIII; Rice as one of two most popular grains in the world. HindIII; Rice as their primary source of and subtropics, rely on rice as their primary source of carbohydrate. Monocytyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumagnashan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice we have constructed a BAC library from oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10,919 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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euphyllophytes, Spermatophyta, Magnoliophyta; Liliopsida, Poales;
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I (bases I to 620)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Contact: Wing RA
Clemson University Genomics Institute
Clemson University
IOU Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Frax: 84 656 4293
Email: rwingelemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                    AQ157444 620 bp DNA GSS 12-SEP-1998 nbxb0009B13r CUG1 Rice BAC Library Oryza sativa genomic clone nbxb0009B13r, genomic survey sequence.
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/organism="Oryza sativa"
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High quality sequence stop: 294.
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AQ157444.1 GI:3554469
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       330 AGTAAGAAGAAGAGGG 346
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                                 High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: 'yahlace@u washington.edu
Clones are derived from the human BAC library RPCI-II. For BAC
Library availability, please contact Pieter de Jong
(pieter@deplong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 957 row: D column: 13
Seq primer: SPG
Class: BAC ends
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis.
1 (bases 1 to 931)
Feng.J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B09381 931 bp DNA GSS 14-MAY-1997
T24A9-Sp6 TAMU Arabidopsis thaliana genomic clone T24A9, genomic
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m c} 179 g 176~{
m t}
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Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
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/db_xref="taxon:9606"
/clone="plate=957 Col=13 Row=D"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 17; DB 82; Length 766; 100.0%; Pred. No. 36; tive 0; Mismatches 0; Indels
99380589
Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 215-899-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
Class: BAC ends
High quality sequence start: 85
High quality sequence stop: 307.
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Location/Qualifiers
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BAC End Sequences at ATGC Unpublished (1997)
Other_GSSs: T24A9-T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B09381.1 GI:2090501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GAGTAAGAAGAAGAGG 27
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Best Local Similarity 100.
Matches 17; Conservative
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B09381
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus. Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Euto 195)

E carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Rahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Rawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Swai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shinakod (1999)

On Jun 5, 1998 this sequence version replaced gi:3188818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-resettc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
please (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA570404 213 bp mRNA EST 09-SEP-1997
nk62g08.s1 NCI_CGAP_Schl Homo sapiens cDNA clone IMAGE:1018142 3',
mRA sequence.
AA570404
AA570404.1 GI:2344384
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 213)
NGI-CBAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
AV011313 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110031J17, mRNA sequence.
AV011313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1110031J17"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 49; I
Pred. No. 1.9e+02;
0; Mismatches 0;
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50 c 33 g 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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100.0%; Pre
0;
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                                                       AV011313.1 GI:4788300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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                                                                                                house mouse.
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   DEFINITION
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1 (bases 1 to 173)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergfelih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1154
Std Error: 0.00
Seq primer: -4UUP from Gibco
High quality sequence stop: 150.
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                                                                                              Length 96;
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
   Dr. Minoru Ko (Wayne State University)." 26 c 26 g 22 t
                                                                                                                                     Indels
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Pred. No. 2.3e+02;
); Mismatches 0;
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                                                                                                                                     16; Conservative
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Best Local Similarity
Matches 16; Conserv
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AV011313/c
LOCUS
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AI278373
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/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
     /db_xref="taxon:9606"
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AQ663218.1 GI:5170986
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Best Local Similarity 100.
Matches 16; Conservative
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AQ663218/c
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                                                                                                                                                                                                                                                                                                                                            CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information be-
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
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clone IMAGE:1893829 3', mRNA sequence.
A1277304
A1277304.1 GI:3899572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index (1997)
Unpublished (1997)
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2287250.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1206
Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                              cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1999
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:637706.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 144.
Location/Qualifiers

    .262
/organism="Homo sapiens"

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Best Local Similarity 100.
Matches 16; Conservative
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-II. For BAC
library availability, please contact Pieter de Jong
(pieter@deforog.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 1039 row: H column: 2
Seq primer: SPG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 263)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ663218 263 bp DNA GSS 23-JUN-1999 HS_5463_B2_D01_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1039 Col=2 Row-H, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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    263
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Location/Qualifiers
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EST.

Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans

Bukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 300)

K Chara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,

Sano, M., Miyada, A. and Nishigaki, A.

Expression map of the C.elegans genome

Unpublished (1996)

On Apr 14, 1993 this sequence version replaced gi:638492.

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

Vata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855
                                                                                            Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Rhazoitina: Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara, Y., Motchashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
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C34963 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk418g1 3', mRNA sequence.
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Location/Qualifiers
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/clone="xk41891"
/clone=lb="xuji Kohara un
hermaphrodite embryo"
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Location/Qualifiers
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65 c 58 g
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C34963.1 GI:2371104
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/ vernick, X.D., Imberski, R.B., and McCutchan, T.F. 1988.
/ Nucleic Acids Research 16:6883-6896). The ends of the
fragments were polished using T4 DNA polymerase, and the
fragments were ligated to EcoR V-cleaved and
dephosphorylated pBlueScript SK(+). Recombinant plasmids
transformed E. coli Xil-Blue."
11 t 16 others
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Plasmodium falciparum
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 272)
Reddy, G.R., Chakrabarti, D., Schuster, S.M., Ferl, R.J., Almira, B.C. and Dame, J.B.
                                                                                                                                                                                                                                                                                                  DNA EST 29-NOV-1993
Roman Reddy Plasmodium falciparum genomic
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Department of Pathobiology
University of Pathobiology
2015 SW 16th Ave., Bldg. 1017, Gainesville, FL 32611-0880
Fax: 352 392 4700
Fax: 352 392 9704
Email: dame@icbr.ifas.ufl.edu
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100.0%; Pred. No. 1.7e+02;
cive 0; Mismatches 0;
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Pred. No. 1.7e+02;
0; Mismatches 0;
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Best Local Similarity 100.
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cenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans.

Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300)

Kohara, Y., Motchashi, T., Tabara, H., Matanabe, H., Sugimoto, A.,

Sano, M., Miyata, A. and Nishigaki, A.

Expression map of the C.elegans genome

Unpublished (1996)

L Contact: Yuj Kohara

Gene Library Lab

National Institute of Genetics

Yata 111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6855
                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa: Metazoa: Rhabditida; Rhabditida;
Eukaryota; Metazoa: Rabditidae; Peloderinae; Caenorhabditis.
Rhabditina: Rabditidae; Rabditidae; Peloderinae; Caenorhabditis.
Expressor in a 300)
Sano, M.; Miyata, A.; and Nishigaki, A.
Sano, M.; Miyata, A.; and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1407336.
Contact: Yuli Kohara
Gene Library Lab
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ychara@lab.nig.ac.jp.

Location/Qualifiers

- Location/Qualifiers

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    300 "Caenorhabditis elegans" / Organism="Caenorhabditis elegans" / Abzrain="Caenorhabditis elegans" / Ab. xref="taxon:6239" / Clone="yk286b3"

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Location/Qualifiers
                C52581.1 GI:2390338
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Caenorhabditis elegans.

Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditidea; Rhabditidae; Peloderinae; Caenorhabditis.

Rhabditina; Rhabditidea; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 300)

KS (Abara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishiqaki, A.

Expression map of the C.elegans genome

Unpublished (1996)

N Sep 12, 1996 this sequence version replaced gi:1400939.

Context: Yul, Kohara

Gene Library Lab

National Institute of Genetics

Yata 111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Medentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Exonno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Kai, C., Fukunishi, Y., Itoh, M., Tawah, M., Kadoka, I.,
Kai, C., Kawat, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Shibata, Y., Salito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Salito, H., Takahashi, F., Tateno, M., Tominaga, N.,
Tsunoda, Y., Watahiki, A., Watahabe, S., Yamamura, T., Yasunishi, A.,
Yockta, T., Yoshik, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1133772.
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Fahabditina: Rhabditidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugimoto, A., Nomoto, H.
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AV332351 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330533L04 3', mRNA sequence.
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On Mar 16, 1998 this sequence version replaced g1:2961756. Contact: Yuli Kohara
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/organism="Caenorhabditis elegans"
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National Institute of Genetics
Yata Lill, Mashima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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/clone_lib="twji Kohara un
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
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/db_xref="taxon:6239"
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                                                               Caenorhabditis elegans. Caenorhabditis elegans
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Mabditina; Rhabditoidea; Rhabditidae; Peloderinae, Caenorhabditis.
(Dases 1 to 300)
Rohara,Y., Shin-i,T., Thlerry-Mieg,J., Thlerry-Mieq,D., Mitsuki,H...
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AV178626 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk569d5 3', mRNA sequence.
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On May 18, 1998 this sequence version replaced gi:3137286.
Contact: Yuji Kohara
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/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied" 89 t 2 others
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/strain="N2"
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National Institute of Genetics
National Institute of Genetics
Tata 1111. Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
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/clone="vk569d5"
/clone=lb="ruji Kohara un
hermaphrodite embryo"
/sex="hermaphrodite"
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The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9018
Email: genome-resertc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
WRI: http://genome.rtc.riken.go.jp,
Iroh,W., Kitsunali. A. Add. Sci. U.S.A. 95 (7), 3455-3460 (1998)
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19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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1. I (Dases 1 to 17799)

1. Muzny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K., Bodeta, B., Bouck, J., Catter, M., Chacko, J., Chen, Z., Cox, C., Burkett, G., Burrows, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, G., Eurado, D., Ding, X., Doman-Rashid, N., Boyld, R., Gorrell, J.H., Jackson, L.E., Jackson, L., Jackson, L., Jackson, L., Luchtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martinez, C., Martinez, C., Morgon, R., Morgues, M., Reiley, D., Baxton, Sparks, M., Senera, J., Borno, M., Sparks, M., Sparks, M., Stamps, M., Sparks, M., Sparks, M., Stamps, M., Sparks, M., Stamps, M., Sparks, M., Sparks, M., Stamps, M., Wabbal, M., Watlington, S., Weinstock, G., Weinschof, I.R., Williamson, A., Worley, K., Wabbal, M., Watlington, Direct Submission

A. Direct Submission

A. On Nov, I7, 1999 this sequence version replaced gi:6249649.

* On Nov, I7, 1999 this sequence version replaced gi:6249649.

* Consists of 97 contigs. The true order of the pieces as soon as it is available and the accession number will

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Worley, K.C.

Direct Submission

Submitted (19-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Dec 10, 1999 this sequence version replaced gi:6478891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-terminator B1g Due: 100% of reads
Assembly program: Phrage; version 0.980611
Consensus quality: 150048 bases at least Q40
Consensus quality: 157979 bases at least Q20
Estimated insert size: 154019; sum-of-contigs estimation
Quality coverage: 5.5x in Q20 bases; sum-of-contigs estimation
                  HTG 09-DEC-1999
*** SEQUENCING IN PROGRESS ***, 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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100845: gap of unknown length
126300: contig of 25455 bp in length
126320: gap of unknown length
145983: contig of 1963 bp in length
146003: gap of unknown length
153267: contig of 7264 bp in length
                                                                                                                                                                                         Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
                                                                                                                                                                       Craniata;
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                  163288 bp DNA
ns clone RP11-764L14,
                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhini
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                                                                                          GI:6552766
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur epm.corn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge,

Washington), Genscan (Chris Burge,

(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), and NetPlantGene

(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), asearches of the complete sequence against a peptide database and the Arabidopsis BST database at TiGR (http://www.tigr.corg/tdb/art/ar.html).

Annotated genes are named to indicate the level of evidence for their annotation Genes with similarity to other proteins are named after the database ints. Genes without significant peptide after the database ints. Genes without significant peptide after the database ints. Genes without protein or EST similarity are named as 'nypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.wustl.edd/dy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/RepeatMasker.html). Regions of genomic sequence that are nonotated as misc features.

Location/Qualifiers

Location/Qualifiers

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Location/Chorber-T2714.1.

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Sc_feature complement(1. .3525).

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Accomplement(1. .3525).
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BAC clone T29E15 is from Arabidopsis chromosome II and is contained
in the YAC clone CIC06C07.
The orientation of the sequence is from SP6 to T7 end of the BAC
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/db_xref="GI:3738314"
/translation="MFLLILLVFCITVFAFVVTNKGAGEAIEGKGYKEYKLGDYSTWL
                                                                                               Direct Submission
Direct Submission
Submitted (13-0CT-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Oct 13, 1998 this sequence version replaced gi:3608124.
Address all correspondence to:
   Medical Center Dr. Rockville, MD 20850, USA, rounsley@tigr.org 3 (bases 1 to 108056)
Rounsley,S.D.
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                                                                                                                                                                                                                                                                          Steve Rounsley
He institute for Genomic Research
9712 Medical Center Dr,
Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"unknown protein,
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1 (bases 1 to 108056)
Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M., Shen, M., Ronning, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C. Arabidopsis thaliana chromosome II BAC T29£15 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 122184 GGAATTTTTGGTTGTGGTCTGTTATCACTAGAAAAATAGATATATTGGTGCTGAAGATA 122125
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Direct Submission
Submitted (23-JUN-1998) The Institute for Genomic Research, 9712
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gap of unknown length contig of 1385 bp in length gap of unknown length contig of 1249 bp in length gap of unknown length gap of unknown length contig of 833 bp in length gap of unknown length
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Direct Submission
Submitted (08-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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/note="exon predicted by xgrail, quality good_shadowexon"
complement(12941. .13003)
/note="exon predicted by xgrail, quality marginal"
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Homo sapiens clone RP11-460B1, *** SEQUENCING IN PROGRESS ***,
unordered pieces.
AC016910.1 G1:6539396
HTG; HTGS_PHASE1.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 161155)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality excellent"
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**NOTE: This is a 'working draft' sequence. It currently consists of I contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                               quality good"
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quality
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                                                        10777. .10792

Inote = exon predicted by xgrail, que complement(11093. .11148)

/note = exon predicted by xgrail, que marginal_shadowexon | 12104. .12164

/note = exon predicted by xgrail, que complement(12288. .13321)

/note = exon predicted by xgrail, que marginal_shadowexon | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 | 12104 
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Pred. No. 0.048;
/note="exon predicted by xgrail,
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                                                                                                                                                                                                                                                                                                                            complement(12754, .12788)
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13060. .13106
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/rpt_family="(CAAAA)n"
13258. .13343
/rpt_family="(TAAAA)n"
        marginal_shadowexon"
10777. 1070
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Waterston, R.H.
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KNRRESEALEHMCKLLGGGGERAKEIAELWREYEENSSPEAKVVKDFDKVELILQALEY
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VTREMFSKESGHVVEETKLRVTYVCSTTTNIISSPRTRRGFIFQCFC"
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//note="exon predicted by xgrail, quality
excellent_shadowexon"
7643. 7711
//note="exon predicted by xgrail, quality excellent"
7643. 7711
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7881. 7943
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842. 843.
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complement(8539. 8578)
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5359. 5475,5691. 3993)

/gene="T29E15.2"
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Complement(3861..319)

/rpt_family="(GAA)n"

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5359. .5475,5694. .5764)
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complement(9146. .9242)
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/note="exon predicted by xgrail,
marginal_shadowexon"
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1959. .2114
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complement(1772. .181
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/gene="T29E15.3"
<6738. .>7603
/gene="T29E15.3"
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Direct Submission
Submitted (03-NOV-1999) Genoscope - Centre National de Sequencage :
Br 191 91006 EVRx cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
Genoscope.

Direct Submission

Submitted (20-CTT-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr
IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence. Work on the sequence is in progress
and the raclease of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                            phage, etc.

contig etc.

contig 8: length 11004 bp

contig 18: length 24666 bp

contig 10: length 24666 bp

contig 10: length 2438 bp

contig 11: length 2471 bp

contig 12: length 2471 bp

contig 12: length 24681 bp

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="matching EMBL:RH99333; Identified using the e-PCR software (G. Schuler)"
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Contig order: 25 21 20 26 30 29 23 27 22 28, 1000 N's separate
segments Contig 25 : length 4440 bp
Contig 21 : length 1785 bp
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HOMe sapiens chromosome 14 clone C-2568PB, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="R-246E14"
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1. .167643
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gaps

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Homo sapiens
Butaryota i Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Cararhini; Hominidae; Homo.

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Connolly, K. S., Gunning, K. M., Davis, C. A., Kadner, K., Subramanian, S., Miguel, T., Lewis, K. D., Fridlyand, J., Alcivare, D., Benke, J. A., Bondoc, M., Bowen, E., Chitang, A., Critz, P., Jaklevic, M. A., Lindo, K., Lindquist, K., Miller, C., Patel, S., Piscia, C., Riley, B. E., Lindquist, M., Sarmiento, R., Yu, C., Montenegro, M., Aerts, A., Chung, A., Abrajano, A., Baker, M., Gau, C., Jett, J., Ko, C., Beall, K., Woolley, J. P., Stultz, J. L., Kimmerly, W. and Martin, C. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence submitted by:
DOE Joint Genome Institute
For further information about this sequence, including its location
and relationship to other sequences, please visit the sequence
archive Website (http://www-hgc.lbl.gov/sequence-archive.html) or
                                                                                                                                                                                                                                                                                                         AC004227 72941 bp DNA PRI 26-FEB-1998

Homo sapiens chromosome 5, P1 clone 356a8 (LBNL H32), complete

sequence.

AC004227 L81383 L81382 L77059 L77058 L81381 L81629 L81804 AC001492

AC0004227 AC000985 AC000983 AC001491 AC000984
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/rpt_family="Alu"
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complement(<2020. .>50956)
/gene="KIA00118-like protein"
complement(join(<2020. .2177,8946. .9186,18985. .19087,
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Rick-D.O. and Wagner.R.P.
Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                      Gaps
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Submitted (26-FEB-1998) Human Genome Center, DOE Joint Genom
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
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Location/Qualifiers
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                    Pred. No. 4.5;
                                                  Mismatches
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complement(1294.
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                                                                                                            93 AAAAATATATATTGGTGC 112
                Best Local Similarity 100.0%; Matches 20; Conservative 0
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="AA034525"
/note="matching EMBL:AA034525; Identified using the e-PCR software (G. Schuler)"
12305. .12491
/standard_name="AA599294"
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to fly@celera.com.
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Adams, M. and Venter, J.C.

Adams, M. and Venter, J.C.

Direct Submission

Submitted (16 NoV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210542 by the submitter.
For further information on this sequence e-mail to fly@celera.cc

* NOTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
Contig 20 : length 1709 bp
Contig 26 : length 12108 bp
Contig 28 : length 32339 bp
Contig 29 : length 62473 bp
Contig 29 : length 2778 bp
Contig 27 : length 2778 bp
Contig 27 : length 1711 bp
Contig 28 : length 1711 bp
Contig 28 : length 23487 bp.
* NOTE: This is a "working draft," sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
16942 a 11043 c 11010 g 16312 t
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367. 484
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complement(24995 .25096)
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/ rpt_family="MER1B"
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/ rote="RAM112" = excellent exon, frame 2"
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31178. 32802
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complement(18985. .19086)
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VEISHPDGKVENLFMGNSFGITFTLDKQYMHGIVRTKVDDCQFVCIAQODYWRILNHT
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LLFRTEQEKSGVPHIPKIAEKKSNRHSIQHVPGDIEQTSQEKGSKKVKANTVSGGRNK
IRKILDKTRESILPPKLFSDGGLSQSQDDSIVGTRHCRHSLAIMPIPGTLSSSSPDLL
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EEFEKNLEDTKMNGHLRLLNIACAARAKWRQVVLQKASRESPLQFSLNGGSEKGFGIF
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13656. .13678
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note="(T)21"
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Birten, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Bulden, D., Balden, J., Barnan, N., Beckerly, R., Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cooke, P., Daly, M.J., Depayre, E., Devon, K., Dewar, K., DuRette, B., Etemadi, S., Ferratia, P., Porrest, C., Gage, D., Gardyna, S., Genshelmer, S., Garagery, K., Gilmartin, T., Gray, D., Hagos, B., Harris, K., Horton, L., Morland, J.C., Hui, L., Jacotot, L., Linton, L., Morland, J.C., Mardis, N., McGurk, A., Meldrim, J., Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D., Roberts, D., Stone, C., Strickland, C., Sydney, K., Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Ye, W.J., Zemtseva, I., Zhao, J. and
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All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Submitted (05-FBB-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
5 (bases 1 to 88071)
                     Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P., Barna, N., Chang, A., Cooke, P., Daly, M.J., Devon, K., Dewar, K., Correst, C., Gage, D., Geralgery, K., Guitau, G., Hagos, B., Huang, J., Jacorott, L., Lane, M., Lee, K., MacKenzie, J., Marquis, N., McDermott, J., Molla, M., Moloney, N., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Peterson, K., Rollins, G., Spencer, J., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Traish, A., Wilmer, F., Zemtseva, I. and Zody, M.
                                                                                                                                                                                                                                                                                                                         Submitted (15-JUL-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 88071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-FEB-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                           AC012680 77340 bp DNA HTG 10-NOV-1999
Arabidopsis thaliana chromosome I clone TAMU-T11111, *** SEQUENCING
IN PROGRESS ***, I ordered pieces.
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Arabidopsis thallana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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1 (bases 1 to 77340)
Lin,X. Kaul,S. Town.C.D., Benito,M., Creasy,T.H., Ronning,C.M., Koo,H., Fulii,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
arabidopsis thaliana 'TAMU' BAC 'Tilill' genomic sequence near marker 'agp64'
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* NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved

* the accession number will be preserved

* the accession number will be preserved
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Homo sapiens chromosome 17, clone HCIT11023, complete sequence.
AC002316
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1 (bases 1 to 88071)

Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone HCITI1023
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Pred. No. 4.3;
0; Mismatches 0; Indels 0
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/db_xref="taxon:3702"
/chromosome="1"
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                                                                                                                                                                                                                                 AC012680.2 GI:6325535
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Lin,X. and Kaul,S.
Direct Submission
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Eukaryota; Meoptera; Endopterygota; Diptera: Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

I (Dases I to 162345)

S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Boyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Richards,S., Sequeira,A., Sethi,H.,
Svirskas,R.R., Wan,K.H., Webster,D., Woolley,P., Yang,S., Yee,M.,
Zieran,L.L. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC006415 162345 bp DNA INV 09-JUL-1999
Drosophila melanogaster, chromosome 2L, region 40B-40C, BAC clone
BACR22A22, complete sequence.
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20480. .20605
20480. .20605
20661. .20703
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/rpt_family="A-rich"
                                            /rpt_family="Aludb"
15832, 16035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t_family="L2"
52.
                                                                                                                                                                                                                                                                                                                                                                                                      complement(23096. .23192)
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complement(23372. .23677)
                                                                                                      /rpt_family="LiMC5"
complement(16350. 16639)
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/rpt_family="Aluxb8"
18830. 18852
/rpt_family="(TAAA)n"
20480. 20605
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complement(26157. .
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/rpt_family="AluSg"
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25644. .25958
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AC006415.11 GI:5430741
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18544. .188
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    .88071
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                                                                                                                                                                                                            680. 701

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complement(0. 796)

/rpt_family="Likh84"

complement(953. 1279)

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/rpt_family="AluSg"/

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1531. 1762
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/rpt_family="AluSq"
4041..4339
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#127. #358

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9305. .9506

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complement(2522. .2784)
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8127. .8358
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152 ATTTACAAGAACAAGTTTG 170
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                             Submitted (19-JAN-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Jul 9, 1999 this sequence version replaced 91:5209360.
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); sequenced by AGOWA within the cDNA
sequencing consortium of the German Genome Project. This clone is
available at the RZPD in Berlin.
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Direct Submission
                  Unpublished (1998)

2 (bases 1 to 162345)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra K., Kearney,L., Kim,E., Lee,B., Lewiss,S., Li,P., Lomotan,M.A., Macda,P., Moshrefi,A.R., Moshrefi,M.Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Sirisks,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
1. .5084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSM800872 5084 bp mRNA PRI 30-AUG-1999 HPMO Sapiens mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163). AL110218.1 GI:5817150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-AUG-1999) MIPS, Am Klopferspitz 18a D-82152
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Sequencing of Drosophila chromosome 2L, region 40B-40C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/strafin="y; cn bw sp"
/db xref="taxon:7227"
/chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (D533)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 100.0%; Pred. No. 3.9; 20; Conservative 0; Mismatches
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32587 c 32005 g 48926 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bdgp@fruitfly.berkeley.edu.
Location/Qualifiers
1. .162345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="40B-40C"
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                                                                                                                                                                                                                                                                                                                                                                   Sequence submitted by:
                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                     Rubin, G.M.
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Matches 2
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HSM800872
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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SOURCE
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OWKKAITILDLODRNTASKYYPLVAQHYASLOBYEIAEELYTKGDRTKDAIDWYTQAG
WRQARKLARKCMRPEDVSYLYITQAGDERGOKYRBAERLYTVTVQEDDAITWYKKH
KLYDDWIRLYGKHHPDLSYTLYITGAGDERGOKARATVNWYRBA
GLWEEAYRVARTQGGANAHKHVAYLWAKSLGGEAAVRLLNKLGLLEAAVDHANDNGSF
BEAELSKLALKHKPPEVHLKYAMFLEBGKREEBAEREIRAKKRKREVALWRYNDOW
BEAAGNYVAEAHDPDSYARVLVGGARGALEKDFGKAEGLLLRAGRPGTALNYKEAGLM
SDALRICKDYVPSQLEALQERFEARTKGGARGVEGALGAROV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVRDSGNSGLAEKĆWMKAĀELSIKFLPPQRNMEVVLAVGPQLIGIĞKHSAAĀELYLNI
DVEKRALDAB TEGEBWNKARVAKELDPRIDPYVDOHYKEREKNGGKVDSLVGYDVIA
ALDILVVEGCQWDKCITETARKQNY KILHKYVALYATHLIREGSSAQALALYVOGGAPAN
PQNFNIYKRIFTDMVSSPGTNCAEAYHSWADLRDVLFNLCENLVKSSEANSPAHEEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTNKSSTIYGTESYVVSLTTNCSGKGILSGHADGTIVRYFFDDEGSGESQGKLVNHPC
PPYALAWATNSIVAAGCDRKIVAYGKEGHMLQTFDYSRDPQEREFTTAVSSPGGGSVV
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VLTVSMDQRLEQVLPRDERGAYEASLVAASTGVRALPCLITGYPILRNKIEFKRPGKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="EDWGDKKVICNKFIQTSAVTCLQWPAEYIIVFGLAEGKVRLANT
/clone="DKFZp434A163"
/clone_ib="434 (synonym: htes3). Vector pSportl; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74673)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                    /note="strong similarity to C. elegans T27B1.1"
/codon_start=3
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                                                                                                                                /tissue_type="testis"
/note="corresponding STS: EMBL:HS09965"
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Homo sapiens clone RG062N11, complete sequence.
AC005683
                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="CaB53678.1"
/db_xref="GI:5817151"
                                                                                                                                                                                                                                                                         /gene="DKFZp434A163"
                                                                                                                                                                                                                       /gene="DKFZp434A163"
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incomplete repeat."
24403. .24786
70ote="LIMD2 repeat: matches 469. .884 of consensus"
24779. .24937
70ote="MER42B repeat: matches 1149. .1300 of consensus"
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32475. .32737
                                                                                                                                                                                                                                                                                                                                                                                                /note-"MLTIB repeat: matches 5. .120 of consensus" 14219. .14506
/note-"match: 216457 STS containing (CA) repeat" 14799. .14319
/note-"20 copies of CA 100 % conserved; differs from 21647; DS2259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32475. .3273/
/note="LiMB1 repeat: matches 566. .302 of consensus"
32859. .33179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5167. .6299
'note="LIME3 repeat: matches 767. .908 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 1. .302 of consensus" 23328. .23478
/note="AluJb repeat: matches 122. .273 of consensus;
                                                                                                                                                                                                                                                                                    1723. .2047

Acte-"match: 267338 STS containing (CA) repeat"

1855. .1877

Anote-"11 copies of CA 100% conserved; differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10571. .11046
/note="MER4A2 repeat: matches 1. .505 of consensus"
11042. .11286
/note="MIRIC repeat: matches 247. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18638. 18929
hotte-"Alusx repeat: matches 302. 6 of consensus"
19749. 20135
/note-"MLTIC repeat: matches 23. .466 of consensus"
                                                                                                                                                                                                                                                           'note="AluJo repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00000 .26282
note="Alufb repeat: matches 293. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alusq repeat: matches 303. .1 of consensus" 31687. .31753
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31926. .32455
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Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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/note="2_copies of 26 mer 98 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9707. .9975
700ce-"MLT1B repeat: matches 390.
70357. .10552
700te-"MLT1C repeat: matches 466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 186.
23026. .23327
                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                      /chromosome="6"
/map="6p22.3-24.3"
/clone="RP3-514K20"
                                                   Location/Qualifiers
                                                                                                                                                                                                             clone_lib="RPCI-3"
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IMPORTANT: This sequence is the entire insert of clone 514K20. During sequence assembly data are compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature be.
                                                                                                              Submitted (15-SEP-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, M. 63108, USA (53108, USA (53108)))))
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                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA PRI 23-NOV-1999
PAC 514K20 on chromosome 6p22.3-24.3. EST,
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514K20 is from the library RPC13 constructed at the Roswell Park
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Eutheria: Primetes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100368)
Wild, A.
                                                                                                                                                                                                                                                       Submitted (05-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MAD 63108, USA.
On May 5, 1999 this sequence version replaced gi:4204336.
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0.0%; Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RG062N11"
14472 c 14794 g 22318
The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .74673
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6p22.3-24.3; repeat polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS514K20 100368 bp
Human DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6100 TTGTGGGTCTGTTATCACT 6118
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                                    2 (bases 1 to 74673)
Waterston, R. H.
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                                                                                            Direct Submission
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HS514K20
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                   JOURNAL
                                                                  AUTHORS
                                                                                                                                                                                     REFERENCE
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.113 of consensus" .268 of consensus"

.256 of consensus"

.1 of consensus"

.386 of

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repeat: matches 298.
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/db_xref="taxon:9606"
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                       61103. .61222
/note="AluY repeat:
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Human DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 82127 GATAATTAGACAAGACAGT 82145
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AL080276.9 GI:5763753
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HSJ101K10/c
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // note="18 copies of 2 mer 89 % conserved"
// note="18 copies of 2 mer 89 % conserved"
// note="Alusx repeat: matches 302. 1 of consensus"
// note="Alusx repeat: matches 15. 297 of consensus"
// note="MATTA2 repeat: matches 1. .149 of consensus"
// note="MATTA2 repeat: matches 1. .149 of consensus"
// note="MATTA1 repeat: matches 1. .365 of consensus"
// note="MATTA1 repeat: matches 154. .374 of consensus"
// note="MATTA1 repeat: matches 154. .374 of consensus"
// note="MATTA1 repeat: matches 154. .374 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    incomplete repett"
39550. 39741
/note="LIMA2 repeat: matches 964. .1055 of consensus"
40095. .40319
/note="LIPA14 repeat: matches 672. .896 of consensus"
41998. .42078
                                                                                                                                                                                                                                                                                                                                39457. .39631
/note="AluJo repeat: matches 125. .299 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MSTC repeat: matches 299. .405 of consensus" 59438. .59525
                                                                                                                                                                                                                                                                                                               .661 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .109 of consensus t
                                                             /note="Alur repeat: matches 1. .298 of consensus" 35042. 35117 /note="MIR2 repeat: matches 146. .74 of consensus" 35186. 35487 /note="Alusq repeat: matches 1. .303 of consensus" 36019. 36447
                                                                                                                                                                                                                           /note="AluSx repeat: matches 302. .1 of consensus" 38520. .38643
/note="MIR2 repeat: matches 145. .16 of consensus" 39015. .39237
/note="LiME1 repeat: matches 432. .661 of consensus" 39457. .39631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /noce="MIR repeat: matches 144. .56 of consensus" 42369. .42595
/note="MERS repeat: matches 1. .230 of consensus" 4264. .42911
/note="Alusp repeat: matches 258. .1 of consensus;
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/note="AluJo repeat: matches 1. .300 of consensus"
43633. .43673
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//note="Alux repeat: matches 1. .301 of consensus" 45157. .45192.
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/note="AluSp repeat: matches 3. .302 of consensus"
53351. .53654
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                                                                                                                                                                                     note="MLTIC repeat: matches 456. .1 of consensus"
88175. .38477
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                           .1 of
                         /note="MLT1C repeat: matches 89.
34014. 34307
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58484. .58593
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42914. .43132
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requests: clonerequest'estager.ac.uk
On Aug 24, 1999 this sequence version replaced gi:5679778.
On hug 24, 1999 this sequence version replaced gi:5679778.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at their source databases:
the entire insert of clone 101K10. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e-g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
This sequence elements (e-g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chf 101K10 is from the library RPCI-1 constructed at the Roswell Park cancer Institute by the group of Pieter de Jong. For further cantains see http://wappic.med.buffalo.edu/ VECTOR: pcyPAC2.
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                              incomplete repeat: matches 2438. 807 of consensus. 61225. 62556. 62807. 62556. 62556. 62807. 62556. 62556. 62807. 62681. 807 of consensus. incomplete repeat: matches 44. 301 of consensus; incomplete repeat. matches 182. 2 of consensus. 6286. 63041. 64784 repeat: matches 297. 1 of consensus. 64497. 64784 folds. 65089. 66144 //note="Wilk repeat: matches 86. 141 of consensus." 66089. 66144 //note="Wilk repeat: matches 86. 141 of consensus." 67000. 67303
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Submitted (28-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire,
CEBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111723)
Phillimore, B.
matches 1. .124 of consensus;
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gap of unknown length
contig of 630 bp in length
gap of unknown length
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Eukaryota; Metazoa Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila;
I (bases I to 116205)
S (Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, R.A., Hummasti, S.R., Karra, K., Kearney, L., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Shif, E., Shif, R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L., and Rubin, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster chromosome 3 clone BACR25A06 (D1082) RPCI-98 23.A.6 map 88E-88E strain y; cn bw sp, *** SEQUENCING IN AC00457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celnker.S.E., Agbayani, A., Arcaina, T.T., Baxter.E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Macda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Shirsky, R.R., Wan, R.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved:
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                                                                                                                                                                                         Length 111723;
                                                                                                                                                                                                                                    0; Indels
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552: gap of unknown length
1038: contig of 486 bp in length
                                                                                                                                                                                    Score 19; DB 11;
Pred. No. 12;
0; Mismatches 0
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Unpublished
  /chromosome="6"
/map="q25-26"
/clone_lib="RPCI-1"
/clone="RP1-101K10"
1 20986 c 21291 g 34007 t
                                                                                                                                                                                    Query Match 9.6%; Sc
Best Local Similarity 100.0%; P:
Matches 19; Conservative 0;
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HTG: HTGS_PHASE1.
fruit fly.
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AC009457/c
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contig of 3420 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 345 bp in length gap of unknown length gap of unknown length contig of 4935 bp in length gap of unknown length gap of unknown length contig of 4939 bp in length gap of unknown length contig of 621 bp in length gap of unknown length gap of unknown length
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.n length
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                unknown length

3 of 865 bp in length

tunknown length

9 of 1811 bp in length

tunknown length
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of 1442 bp in length
k unknown length
of 1636 bp in length
unknown length
of 1815 bp in length
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of 603 bp in length
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of 1109
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Direct Submission

Note that the Sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, graft, sequence from E.coli, graft, sequence from E.coli, graft, vector, phage etc. Order of sequence from E.coli, yeast, vector, phage etc. Order of sequence from E.coli, yeast, vector, contig_ID 00000 Length: 12284bp
Contig_ID: 00000 Length: 14293bp
Contig_ID: 00000 Length: 3107bp
Contig_ID: 00000 Length: 3107bp
Contig_ID: 00000 Length: 3107bp
Contig_ID: 00000 Length: 3107bp
Contig_ID: 00000 Length: 3202bp
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                     AL133269 128247 bp DNA HTG 03-DEC-1999 HOMO sapiens chromosome 6 clone RP3-468K3 map q25-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128247)
Plumb, B.
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Pred. No. 12;
0; Mismatches 0; Indels 0;
                     41; Length 116205;
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                  DB 4
                  Score 19; DB 4
Pred. No. 12;
0; Mismatches
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/db_xref="taxon:9606"
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100.0%; Pre
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Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
                                                                                                                                                                    Db 16478 CTAGAAAATATATATT 16460
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HTG; HTGS_PHASE1.
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                                                                                                                                  89 CTAGAAAAATATATATT 107
               Query Match
Best Local Similarity 100.
Matches 19; Conservative
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TITLE
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20691: contig
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25939: contig

26843: contig

26843: gap of

27743: contig

gap of

28649: contig

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Lirect Submission

All repeats were identified using RepeatMasker:

Sall repeats were identified using RepeatMasker:

Sall, A.F.A. & Green, P. (1966-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center project Information

Center clone name: 45_A.9
                                                  AC015596 135711 bp DNA HTG 17-NOV-1999
HOMO saplens clone RP11-45A9, LOW-PASS SEQUENCE SAMPLING.
AC015596
AC015596.1 GI:6447091
HTG: HTGS_PHASE0; NULL.
                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 135711)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-45A9
Unpublished
2 (bases 1 to 135711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This record contains 154 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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9 of 854 bp in length

t unknown length

9 of 829 bp in length

t unknown length

9 of 866 bp in length
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f unknown length
g of 865 bp in length
f unknown length
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of 861 bp in length
unknown length
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                                                                                                                        human.
                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                      RESULT 18
AC015596
LOCUS
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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Submitted (03-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: olonerquest@sanger.ac.uk
requests: olonerquest@sanger.ac.uk
no Dec 3, 1999 this sequence version replaced gi:6491758.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
contig_ID: 00362 Length: 1040bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154129)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
                                                             Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152583)
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*** SEQUENCING IN PROGRESS ***, 23
                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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100.0%; Pred. No. 12;
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/map="q42.13-43"
/clone="RP4-709L21"
/clone="lb="RPC1-4"
1 31061 c 33040 g 43820 t
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124660bp
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Length: 4631bp
Length: 1796bp
Length: 1585bp

    11. 152583
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Length: 1966bp
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AC009427.1 GI:5757602
HTG; HTGS_PHASE1.
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Contig_ID: 0098
Contig_ID: 01010
Contig_ID: 01728
Contig_ID: 01728
Contig_ID: 02108
Contig_ID: 02181
Contig_ID: 02245
Contig_ID: 02591
Contig_ID: 02591
Contig_ID: 02591
Contig_ID: 02591
Contig_ID: 02591
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AL078646
AL078646.20 GI:6
HTG; HTGS_PHASE1.
                                                                                                      Donnelly, S.
Direct Submission
                                                     Homo sapiens
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VERSION
KEYWORDS
SOURCE
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AC009427
                                                                                          REFERENCE
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g unknown length
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g of 879 bp in length
miknown length
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g of 862 bp in length
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                of 882 bp in length
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Pred. No. 12;
0; Mismatches
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REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Clone RG242H14 is from a release of the human BAC library
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Marquis, N., McDwan, P., McGurk, A., McKernan, K., McLaughlin, J., Maldrim, J., Molla, M., Oconnor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Kiley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfey, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                               Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

**This is a 'working draft' sequence. It currently consists of 23 confligs. Thus of Action order of the pieces is not known and their corder in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
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contig of 21408 bp in length
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director). John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see this sequence, she http://www.nhgri.nih.gov.vor/DIR/CIB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-JUN-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA SUBMITTED BY: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate commistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC005165 155164 bp DNA PRI 20-JUN-1998
Homo sapiens BAC clone RG242H14 from 7p15-p21, complete sequence.
AC005165
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155164)
Becker, M., Tin Wollam, A. and Harrison, M.
The sequence of Homo sapiens BAC clone RG242H14
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                                                                                                                                                                                                                                                                                                                                                                           DB 41; Length 154129;
12;
gap of unknown length
Location/Qualifiters
1. 154129
/organism="Homo sapiens"
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40465 a 35517 c 34138 g 42930 t 1079 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 4
; Pred. No. 12;
0; Mismatches
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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confirmed by restriction digest.
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2 (bases 1 to 155164)
Waterston, R.
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Best Local Similarity 100.0
Matches 19; Conservative
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CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                     NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RG241102, 200 bp overlap.
Actual start of this clone is at base position 88412 of RG241102;
actual end is at 155164 of RG242H14.
Location,Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(26404. .26808)
/note="ubiquitin/CEP52 pseudogene"
complement(26727. .26811)
/note="match to EST AA368309 (NID:g2020628)"
27675. .28202
                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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10198 .10511
/rpt_family="MER1_type"
11312 .11486
/rpt_family="MIR"
11916 .12524
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/rpt_family="Retroviral"
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complement(2701. .3012)
/db_xref="GI:1916422"
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195. .455
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|/rpt_family="(TGAA)n"
|754. .1805
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267. .383
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/rpt_family="L1"
24656. .24824
/rpt_family="MaLR"
24825. .2512
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/rpt_family="MIR"
18811. 18986
/rpt_family="L2"
21003. 21003
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/rpt_family="MIR"
j139. .119A
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/18519. 186/1
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6744. 6897
/rpt_family="MIR"
                                                                           chloramphenicol
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25178. .2537
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?6231. >=>=
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1900. .2827
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/rpt_family="Alu"
9828. .10013
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/rpt_family="MIR"
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/rpt_family="MIR"
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16979. .17281
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Direct Submission

L Submitted (06-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
ON Apr 16, 1999 this sequence version replaced gi:4371318.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as it in so of N, but the exact sizes of the gaps are unknown.

* This record will be exact sizes of the finished sequence as soon as it is available and the finished sequence as soon as it is available and the accession number will be preserved.
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Homo sapiens clone DJ0832014, *** SEQUENCING IN PROGRESS ***,
unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

( Dases I to 166925)
Waterston, R. H.
The sequence of Homo sapiens clone
Unpublished
2 (bases I to 166925)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                       42; Length 158454;
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42130: contig of 8066 bp in length contig of 8066 bp in length gap of unknown length le52935: contig of 10805 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length lo0212: contig of 13572 bp in length gap of unknown length gap of unknown length lo2923: contig of 22711 bp in length gap of unknown length gap of unknown length la58454: contig of 35531 bp in length gap of unknown length length
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1. :158454
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="115="I_3"
/clone=lib="RPCI-11 Human Male BAC"
a 28914 c 28662 g 49852 t
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Matches 19; Conservative
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Homo sapiens clone 115_I_3, *** SEQUENCING IN PROGRESS ***, 14
unordered pieces.
                                                                                                                      Gaps
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1 (bases 1 to 158454)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone 115_1_3
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                                                                                    DB 11; Length 155164; 12;
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100.0%; Pred. No.
 /rpt_family="MIR"
58356. .58574
/rpt_family="MIR"
60264. .60469
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.0
Matches 19; Conservative
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AC011107/c
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KEYWORDS
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Gaps

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Homo sapiens chromosome 3q27 clone RP11-119E3, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.

AC012149
AC012149
AC012149
AC012149.1 GI:6091636
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 192823)
NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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unknown length
of 13527 bp in length
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of 20923 bp in length
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/db_xref="taxon:9606"
/chromosome="3"
/map="3"
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens chromosome 3 clone RP11-573D15 map 3, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
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Center Droject Information
Center Droject Information
Sequencing vector: M13; M7815; 100% of reads Sequencing vector: M13; M7815; 100% of reads Chemistry: Dye-terminator B19 Dye: 100% of reads Assembly program: Phrap: version 0.960731
Consensus quality: 159143 bases at least Q40
Consensus quality: 159324 bases at least Q20
Insert size: 182000; aqarose-fp
Insert size: 174050; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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HTG: HTGS_PHASE1: HTGS_DRAFT.
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       Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Buxiekt, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frandac, D., Hodgson, A., Hogues, M., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kowar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nelson, A., Nguyen, N., Nguyen, S., Oswal, G., Raish, B., Paxcon, S., Paylon, B., Parez, L., Pu, L. L., Quiles, M., Raish, B., Paxcon, S., Paylon, B., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Volo, Wahbah, M., Watlington, S., Neinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., L., Warlestock, G., Weinstock, I.R., Williamson, A., Worley, K., Mren, J., Showitson, R., Chore, G., Melission

Al, Unpublished

Direct Submission

Submitted (21-OCT-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

* NOTE: This is a "working draft' sequence record is a soon as it is available and the contegs are represented as trus of N. but the exact sizes of the flashed sequence

* as soon as it is available and the contegs are represented as trus of the preserved.
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25 127870: contig of 2:
71 157857: contig of 2:
58 192823: contig of 3:
Location/Qualifiers
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81 others

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42230 c 42416 g 54504

53592 a

BASE COUNT ORIGIN

/clone="RP11-119E3"

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Leases I to 231949)

Blackey, S.

Blakey, S.

Blater, Cablandsion

Submitted (08-0cr1999) Wellcome Trust Genome Campus, Hinxton, Cambridgealire, CB10 1524, WK. E-mail enquires:

Combridgealire, CB10 1524, WK. E-mail enquires:

humquery@anager.cuk Clone requests: clonerequest@anager.ac.uk

no Oct II, 1999 this sequence is unfinished and does not necessarily

represent the correct sequence in unfinished and does not necessarily

represent the correct sequence in work on the sequence is in progress

and the release of this data is based on the understanding that the

sequence may change as work continues. The sequence may be

contaminated with foreign sequence from E.coli, yeast, vector,

phage ecc. octor of sequence 130109015 Contig_ID: 00002

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by Unfinished: dJ1099015 Contig_ID: 00040 acc_ALO35456

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acc_ALO35456 Length: 1370 by Unfinished: dJ1099015 Contig_ID: 0280

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                                                                      Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 231949)
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DB 43; Length 192823;
11;
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   9.6%; Score 19; 100.0%; Pred. No.
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PWIPCTSQVWTQAITFYASSLCSIFAFCTLVYAFITSDFSVQNVFLHSSTLKPLIYKI
SGSWSSHEGSMLAWFCLLQIVSCCYIFCLEDKMLKFSSIIILSAIQLLFSSFIYFTSN
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MINNGQIIGDKKNIIALSLGSDNSIIVNANTLYSGIRTTKNNQGTVTLSGGMPNNPGT
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              EDQIYGEKLEIHEILKDPNNAAENFKKYVSQISRQFKKDLDKDQKNHIDSNFNTQKVI
NDSNKDIQVEHITSYVQDKEKOSKPQGFLTRIFNYFKNIVFKQ"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA15139.1"
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3341. F2
                                                                                                                 /gene="RP702"
2074.
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                                                                                                                                                                                            2074. .3348
/gene="RP702"
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/gene="RP703"
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ALPONSELKSYWKQIIEKVDHVFFTNBADQNLSIADGIVPKDKTTTITDIRLVISVFN
NLIYNHETNHGLSSTIYKKVDKLIKTAKNQDSKEIIETWPISVDBATNLITAKFGITS
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Anderson, S.G.E.

Direct Submission

Submitted (11-NOV-1998) S.G.E. Andersson,

Siv. Andersson/amolbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S.T51 24, SWEDEN
bp Unfinished: dJ1099D15 Contig_ID: 03081 acc=AL035456 Length: 1537 bp Unfinished: dJ1099D15 Contig_ID: 03084 acc=AL035456 Length: 1084 bp Unfinished: dJ1099D15 Contig_ID: 03283 acc=AL035456 Length: 7634 bp Unfinished: dJ1099D15 Contig_ID: 03255 acc=AL035456 Length: 2178 bp.
* NOTE: This is a "working draft' sequence.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPXXO4 237523 bp DNA BCT 11-NOV-1998 Rickettsia prowazekii strain Madrid E, complete genome; segment
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Complete genome.
Rickettsia prowazekii
Rickettsia prowazekii
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Rickettsia prowazekii
Rickettsiaceae: Rickettsiaee; Rickettsiaees;
Rickettsiaceae: Rickettsiaees;
1 (bases 1 to 237523)
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100.0%; Pred. No. 11;
Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .231949

/organism="Homo sapiens"

/db xref="taxon:9606"

/chromosome="20"

/chromosome="20"

/clone="11b="RPCI-5"

a 42805 c 43044 g 58039 t 29631 others
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/organism="Rickettsia prowazekii"
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/db_xref="taxon:782"
164. .1123
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164. .1123
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les 19; Conserv
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RPXX04/c
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SOURCE
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l (bases 1 to 1563)
Robert, L.S., Allard, S., Franklin, T.M. and Trick, M.
Sequence and expression of endogenous S-locus glycoprotein genes in self-compatible Brassica napus
Mol. Gen Genet. 242 (2), 209-216 (1994)
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TEKISHASLULLDQSDTTWASTNLTGVALLEWTAELLANGREVLENSKTNDLDRFWWO
SEDYPWDTLLEPAKTGRKHKSSERRKILTSWKSPTDPSSGDYSLILETEGFLHEFYLE
KNEFKVYRTGPWNGVRFUGIPKKMOWNSYIDNSFIDNNEEVAYTFKVHNNNMIHSRF
RMSSTGCYLOYTWATRYPQRNNEWSPEDTOOLYKVGGPAFACDMHTSPTCNCIKGFV
RMSSGRWDLKDMSGGCYRSKLSCGEGGGFLEMSOWKLPETSBALVERRIGKECREK
CVRDGNGTGYANMDLKDGGGGCVSSKLSCGEGGGFLEMSOWKLPETSBALVERRIGKECREK
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/db_xref="G1:"Gab1246"
/translation="MSIEKEKFWASHKQVVKEIGGINLINGKHDLFRAVAYTSDDIEA
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/protein_id="AAA70399.1"
/db_xref="G1:44112"
/translation="MKGVIPHYHHSYTFFFVILVLFPHAFSTNTLSSNEALTISSNKT
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/note="pseudogene with one authentic frameshift. Homology to resolvase."
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Brassica napus S-locus related protein (SLR-WS-1) mRNA, complete
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Robert, L.S.
Direct Submission
Submitted (11-FEB-1994) Laurian S. Robert, Agriculture Canada,
Plant Research Centre, Ottawa, Ontario, K1A OC6, Canada
Location/Qualifiers
1. 1563
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100.0%; Pred. No. 11;
1ve 0; Mismatches 0; Indels 0
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                                                                                                             /gene="RP712"
complement(22602. .23066)
/gene="RP712"
/codon.start=1
/transl_table=11
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                                                                                  complement(22602. .23066)
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/sub_species="oleifera"
/db_xref="taxon:3708"
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/gene="SLR-WS-1"
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/codon_start=1
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14. .1354
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L10737.1 GI:484111
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Best Local Similarity 100.
Matches 19; Conservative
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VERSION
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AUTHORS
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TITLE
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BNASLRGA
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complement(15220. .15507)
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complement(19685. .20789)
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                                                                                                                                                                                                                                                                 /note="Pseudogene that lacks ATG or GTG initiation codon. Homology to guanosine-3,5-bis(diphosphate)
3-pyrophosphohydrolase."
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complement(13563. .14507)
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/product="5LH_GENERAL CONTROLL CONTROLL
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Submitted (22-FEB-1994) Oldknow J., Cambridge Laboratory, Institute
of Plant Science Research, Brassica & Oilseeds Research, John Innes
Centre, Colney Lane, Norwich, Norfolk, UK, NR4 7UJ
3 (bases I to 1794)
Oldknow,J., Franklin,T.M., Allard,S., Robert,L.S. and Trick,M.
DNA sequences of the two homoelogous SLR1 genes of Brassica napus
cv inestar
                                                                                                                                                                                                                             Direct Submission
Submission (13-07-1993) Oldknow J., Cambridge Laboratory, Institute of Plant Science Research, Brassica & Oilseeds Research, John Innes Centre, Colney Lane, Norwich, Norfolk, UK, NR4 7UJ
revised by [3] MAT
2 (bases I to 1794)
                                                                         Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Brassica.
1 (bases 1 to 1794)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sex. Plant Reprod. 8, 254-255 (1995)
On Feb 23, 1994 this sequence version replaced gi:407774.
Location/Qualifiers
1. .1794
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1538. .1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Stigma"
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142. 1476
Z26914.1 GI:456316
SLR1 gene; SLR1 glycoprotein.
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Best Local Similarity 100.
Matches 18; Conservative
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PKNAGRWDLRDMSGGCVRSSKLSCGEGDGFLRMSQMKLPETSEALVEKRIGLKECREK
CVRDCNCTGYANMDIMDGGSGCVTWTGELVDMRKYDAGGQDLYVKVAEASLVPS"
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons;
Rosidae: Capparales: Brassicaceae: Brassica.
1 (bases 1 to 1563)
20ldrow, J., Franklin, T.M., Allard, S., Robert, L.S. and Trick, M.
DNA sequences of the two homoelogous SIRI genes of Brassica napus
cv inestar
                                                                                                                                                                                                                                                                                                                                          B.napus mRNA for endogenous S-locus glycoprotein (cone SLR1-Ws-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert, L.S.
Direct Submission
Submitted (05-FEB-1993) Robert L. S., Agriculture Canada, Plant
Research Centre, 960 Carling Avenue, Ottawa, Ontario, Canada, KlA
OC6
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Pred. No. 71;
                                                 Length 1563;
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B.napus (Westar) SLR1 gene for SLR1 glycoprotein.
226914
                                              Score 18; DB 7; Pred. No. 71; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          endogenous S-locus glycoprotein gene.
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2 (bases 1 to 1563)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Westar"
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/clone="SLR1-Ws-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="glycoprotein"
/protein_id="CAA79735.1"
/db_xref="GI:2285899"
                                                   Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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ilarity 100.0%; P
Conservative 0;
                                                 Query Match

9.1%; So
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
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1879 GAAAATATATATTGG 1896
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Fidock, D.A.
Direct Submission
 (bases 1 to 2139)
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Best Local Similarity 100..
These 18; Conservative
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PFSTARP/c
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DODSYLCNYTLERKAVDDERHKARENKTIVRDFOYNBEDEMARNEEMPELSTDKKKQF
GPLVRWLKVNFSERTEMIHIKALRVPVESVLRYGLPVNFQAMLLOPRKKSVKKLREV
LHELYKHLDSSAAAIIDAPMDIPGLNLSQQEYYPYVYKIDCNLLEFK"
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (19-AUG-1994) Gary E. Dean, Mol. Genetics, Biochemistry, and Microbiology, University of Cincinnati College of Medicine, 231
Bethesda Avenue, Cincinnati, OH 45267-0524, USA
Location/Qualifiers
1. 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="WTEFWLISAPGERTCOOTWERLHAATTKNNNLAVSSKFNIPDLK
VGTLDVLVGLSDELAKLDAFVEGVVKKVAQYMADVLEDSKDKVQENLLASGVDLVTYI
TRFQWDMAKYPIKQSLKNISEIIAKGVTQIDNDLKSRASAYNNLKGNLQNLERKNAGS
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euphyllophytes: Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae: Capparales; Brassicaceae; Brassica.
1 (bases 1 to 2139)
Trick, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-MAR-1990) Trick M., Cambridge Laboratory, John Innes
Centre for Plant Science Research, Colney Lane, Norwich NR4 7UJ, U
K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //note="subunit C, V-ATPase"
/codon_start=1
/evidence=experimental
/product="vacuolar adenosine triphosphatase subunit C"
/protein_id="AAC83084.1"
/db_xref="GI:3955098"
MMU13839 1825 bp mRNA ROD 03-DEC-1998
Mus musculus vacuolar adenosine triphosphatase subunit C mRNA,
complete cds.
                                                                                                                                    Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1320)
Howell, M.L. and Dean, G.E.
CDNA sequences for mouse vacuolar ATPase subunits
Unpublished
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Pred. No. 70;
0; Mismatches 0; Indels
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Brassica gene for S locus related glycoprotein. 252089 GI:17896
S locus related glycoprotein: secreted protein. Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="vacuolar acidification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 t
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="ES-D3"
/dev_stage="18.5 day"
156. 1304
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                     U13839.1 GI:3955097
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                                                                                                                          house mouse.
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/db_xref="G1:17897".1"
/db_xref="G1:17897".1"
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/db_xref="Swiss-PROT: PROGRAMMARDALHOWG
TLVSGDVFECGFETTTRNSPGTORNY.COMWARDALHOWG
TLKISHASLVLLDHSNTPFPWSTNFTGVAHLEVTAELLANGNFVLRDSKTNDLDRRWG
TLKISHASLVLLDHSNTPFWSTNFTGVAHLEVTAELLANGNFVLRDSKTNDLDRRWG
TKNTSTROFWIGVRENGIFKMGWNSTLITSWKSPTDPSSGDFSFILETEGFLHFFYLL
KNEFKYYRTGPWIGVRENGIFKMGWNSTSTDSKILDNEEDAXFORNNNHHTRFRM
SSTGILQVITWTRTVPQRNMFWSFPEDTCDLYKUGPYAYCDMHTSPTCNIKGFVPK
NAGRWDLRDMSGGCVRRSKLSGGEGFERNSGWKLDETSBAVUNKIGFLKECREKCV
RDCNCTGYANMDIMNGGSGCVWWTGELDDMRKYNAGQDLYVKNAAASLVPS"
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TION P.falciparum gene for STARP antigen.

226314.1 GI:499324

35 TARP antigen.

Plasmodium falciparum

Plasmodium falciparum

Plasmodium falciparum

Pokaryota, Alvolata; Apicomplexa; Haemosporida; Plasmodium.

CE 1 (bases 1 to 2787)

RS Foliock,D.A., Bottius,E., Brahimi,K., Moelans,I.I.M.D., Alkawa,M.,

RCOINGS.R.N.H., Certa,U., Olafsson,P., Kaidoh,T., Asavanich,A.,

Guerin Marchand,C. and Drullhe,P.

Cloning and characterization of a novel Plasmodium falciparum

sporocite surface antigen, STARP

SSOL1993
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Trick,M.
Genomic sequence of a Brassica S locus-related gene plant Mol. Biol. 15 (1), 203-205 (1990)
91355861
Data Kindly reviewed (02-JUN-1990) by Trick M.
Location/Qualifiers
1. 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2139;
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/product="signal peptide (AA -28 to -1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463. .1710
/product="mature peptide (AA 1 to 416)"
1775. .1780
                                                                                                                                                                                    /organism="Brassica oleracea"
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/clone="lib="blanbda EMBL4"
/clone="BS63-1"
/clone="BS63-1"
/clone="Tara box"
329. .335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 7;
Pred. No. 68;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   329. .335
/note="TATA box related"
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409 c 446 g
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100.0%; PI:
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//translation="WATPLSISSNPLTSRHCYRLHLSSTSFKGNVSVLGANPSGILSS.
//translation="WATPLSISSNPLTSRHCYRLHSPREADMLGPQPGSRKKQKRKGRG
ISAGQGASCGFGMRGQKSRSGPGIMRGFEGGGTALYPRLPKILGTGGAGMRGGIPKYLP
VNIKDIETAGFQFQCDDFSLETLKQKGLINPGSREKLPLKILGTGELSMKLFFRARAF
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                                                                                                                                                                                                                    /citation=[2]
/function="This mRNA encodes plastid ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                              /citation=[2]
/function="Encodes chloroplast ribosomal protein CL15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(1231. ..1314,1386. .1749,2042. .2193,2288. .2521)
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                                                                                                                                                                              .1749,2042. .2193,2288. .2678)
                                                                                                                                                                                                                                                                                                                                                   nuclear gene that encodes plastid CL15. This gene has 4 exons and 3
                                             On Mar 27, 1995 this sequence version replaced gi:16496 Location/Qualifiers
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                                                                        FEATURES
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NNNTTTNTSTTENNNINTNTNNSTENTSATKKVTENVITNQILIGNNNTTTNTSTTEH
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TDNNYKTISTDNNNTKTISDNNNTKTISTDNNNNTNRQYVFANNYNETTSDBELNK
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Submitted (16-SEP-1993) David A. Fidock, Laboratory of bio-medical parasitology, Pasteur, Institute, 25, rue du Dr. Roux, Paris, PARIS, 7574 CEDEX 15, France
Location/Qualifiers
1. 2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Spermatophyta: Agnoliophyta: Spermatophyta: Rosidae: Capparales: Brassicaceae: Arabidopsis.

[ (bases 1 to 2984)
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Thompson,M.D., Jacks,C.M., Lenvik,T.R. and Gantt,J.S.
Characterization of Frs17, rp19 and rp115: three nucleus-encoded plastid ribosomal protein genes
                                                                                                                                                                                                                  /dev_stage="Sporozoite, liver stage, erythrocytic ring stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATRPCL15G 2984 bp DNA PLN 21-MAR-1995 A.thaliana rpl15 gene for plastid ribosomal protein CL15. 211508.1 G1:732561 ribosomal protein: ribosomal protein: ribosomal protein: ribosomal protein: ribosomal protein.
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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Direct Submission
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DEFINITION
ACCESSION
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ATRPCL15G/c
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AUTHORS
TITLE
JOURNAL
         JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (mtbC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF102623 7186 bp DNA BCT 24-MAY-1999 Methanosarcina barkeri dimethylamine corrinoid protein MtbC (mtbC), trimethylamine methyltransferase MttB (mttB), trimethylamine corrinoid protein MtC (mttC), putative transmembrane protein MttP (mttP), and dimethylamine methyltransferase MtbBl (mtbBl) genes, complete cds.
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9 (bases 1 to 7186)

Paul, L. and Krzycki, J.A.

The genes encoding the trimethylamine and dimethylamine methyltransferases of Methanosarcina barkeri are cotranscribed and interrupted by translationally bypassed in-frame amber codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferguson, D.J. Jr. and Krzycki, J.A.
Reconstitution of trimethylamine-dependent coenzyme M methylation with the trimethylamine corrinoid protein and the isozymes of methyltransferase II from Methanosarcina barkeri
J. Bacteriol. 179 (3), 846-852 (1997)
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Ferguson, D.J., Gorlatova, N., Paul, L., Grahame, D. and Krzycki, J.A.
The corrinoid protein from Methanosarcina barkeri specific for
dimethylamine: CoM methyl transfer
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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734. .1375
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0
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red. No. 65;
Mismatches 0;
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Submitted (27-0CT-1998) Microbiology, C
West 12th Ave. Columbus, OH 43210, USA
1. 7186
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100.08; Pre
0;
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4 (bases 1 to 7186)
Paul, L. and Krzycki, J.A.
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Methanosarcina barkeri
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AF102623.1 GI:4262423
               /gene="rpl15"
/citation=[2]
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734. .1375
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1 (bases 1 to 7186)
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Best Local Similarity
Matches 18; Conserv
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AF102623
LOCUS
DEFINITION
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TYAAQASSGQATHWIAKVPEGSNLGGSDQGTAKLNTITDFRDQANSIFAIDKOGNKUD
FYDALGKELSPSENRKASFTESSISEKMKGAGFKVLKEKKKELLDEFFKEGKITDPER
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3532. . 4677
                                                                                                                                                                                                                                                                                                                                                                                                           AKDFWYSWLRTYSRNLEYRLNTGGSKELDEALKSKLAEENSPVYGEOWSFGNIYTYAL
FGIDANKLEFKDKFTQKVSAEGNIKDREATIFESINGKEKDANISSFFESQFASGTYD
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FISSKLGKNYKFNENFAKLVYGSSLADIDSGKADTSESYLFGKGLSFRTLLYAAVNWD
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NNPNSALYINMAKLEFTPLQYSLIIIVPTFFISSILGIAIGVIAGYKRGKWFDVSSNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"oligopeptide transport system permease
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                         /clone="HIII-13"
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631. .3516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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3532. .4677
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4679. .5953
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                                                                                           /gene="P100"
631. 3516
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/gene="oppD"
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1 (bases 1 to 10414)

Henrich, B., Hopfe, M., Kitzerow, A. and Hadding, U.
The adherence-associated lipoprotein P100, encoded by an opp operon structure, functions as the oligopeptide-binding domain OppA of a putative oligopeptide transport system in mycoplasma hominis

J. Bacteriol. 181 (15), 4873-4878 (1999)
/note="UAG codon is translated by an undetermined
mechanism: ORF identified by N-terminal sequence of 50 kDa
DMA methyltransferase polypeptide"
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1. 10414
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Duesseldorf, Universitaetsstrasse 1, 40225 Duesseldorf, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mycoplasma hominis P100, oppB, oppC, oppF genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; Length 7186;
Pred. No. 57;
0; Mismatches 0; Indels
                                                             /codon_start=1
/transl_except=(pos:6535. .6537,aa:0THER)
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/clone="EI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                       LLDIKINSCNLFRKQIA"
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MHX99740/c
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/codon_start-1
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/gene="M18.3"
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                                                                                                                                                                                  Direct Submission
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268507.1 GI:1159944

HTG: Collagen: DNA repair protein like; Dyenin like.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa: Nematoda: Secernentea; Rhabditia; Rhabditida;
Rhabditiona; Rhabditodea: Rhabditidae: Peloderinae. Caenorhabditis.
1 (bases 1 to 26542)
Wilson,R., Ainscough,R., Anderson,R., Baynes,C., Berks,M.,
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Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., Refken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Stadden,R., Waterstyn,A., Weinstock,L., Vauddin,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFFEYVEÖLRÖKEKDKILLKIAELKONODKSNKDKKSLAKLOSKLÄSIKVOYNTILKM
YHSDISLKEDTLKSFDIERKYLDKDINNIYVLLGIDHKWVETNLKTADAMAGVDAKHM
KWWWRRRYFDSKVSYPIAKLLISSILYKTIIYKALEDVGLLKÖFAYRYPHEFSGGGLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIVIARALIVEPOVIVADEPIASLDISIQAQVVNLLKELCIKKNIGLIFIAHDLSMIE
YVADEVQIMHLGKIVESGKTEAIYANPIHPYIINLEKAIPKISNANEKFQNVSFALDY
LDEQKFPNVPETFKODYVVGTTASQIKQWTHNAKLEKEHKEL"
1415 C 1501 g 3341 t
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forcoduct="oligopeptide transport ATP-binding protein
formolog"
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/product="oligopeptide transport ATP-binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 1; Pred. No. 54; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"SPTREMBL:053112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA68077.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.18;
                                                                                                                                                                                                                                                                                                                   7114. .9642
/gene="oppF"
7114. .9642
/gene="oppF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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DEFINITION
ACCESSION
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CEM18
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ORIGIN
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KEYWORDS
SOURCE
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Current sequence finishing criteria for the C. elegans genome current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone M18. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone M18 is at 1 in this sequence. The true right end of clone M18 is at 10009 in sequence. The true right end of clone B00001 is at 26439 in this sequence. The true right end of clone B0001 is at 23200 in this sequence. The true right end of clone F11A10 is at 23200 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / COLOUS_START 13878765"

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/ Ab_Xref="G1:3878765"

/ Ab_Xref="SPTREMBL:021555"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-1996) Louis, MO 63110, USA. E-mail:
Les Gesnger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
Wilkinson-Sproat, J. and Wohldman, P. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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cDNA EST EMBL:D70719 comes from this gene; cDNA EST
EMBL:D66790 comes from this gene; cDNA EST EMBL:D65910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        available information.
For a graphical representation of this seguence and its analysis
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8050. 8308)
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/gene="M18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=M18
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/chromosome="IV"
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5816. .8308
                                                                                                                                   elegans
Nature 368 (6466), 32-38 (1994)
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REFERENCE
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comes from this gene; CDNA EST EMBL:D65830 comes from this gene; CDNA EST EMBL:D66173 comes from this gene; CDNA EST EMBL:D650704 comes from this gene; CDNA EST EMBL:D650704 comes from this gene; CDNA EST EMBL:D65111 comes from this gene; CDNA EST EMBL:D65811 comes from this gene; CDNA EST EMBL:D65811 comes from this gene; CDNA EST EMBL:D6581 comes from this gene; CDNA EST EMBL:D66581 comes from this gene; CDNA EST EMBL:D66904 comes from this gene; CDNA EST EMBL:D69913 comes from this gene; CDNA EST EMBL:D69813 comes from this gene; CDNA EST EMBL:D69813 comes from this gene; CDNA EST EMBL:D70031 comes from this gene; CDNA EST EMBL:D69810 comes from this gene; CDNA EST EMBL:D70037 comes from this gene; CDNA EST EMBL:D70037 comes from this gene; CDNA EST EMBL:D1046 comes from this gene; CDNA EST EMBL:C11746 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASTLFGPNDSGIILQATEKOIRLMSSSGLSKFWEPTNGEIISKVSVNAANGQIVLAA
RDTVYLLITCIVDEMGALDIQLTAEKKFENEIACLDLSNEGDDPNNKATFLVLAFFWSTF
AMEVIQLPDLIIVCHTDLPTKIIPRSIIATCIEEVHYLLVAFGDGALVYVYFDIKTGT
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CIADPTGRATDNLFSLTIHRNGLIAIRAFEGSVKMIQWESGTDLRHFNVRFDYPNVSD
FKFVDTGEDDVYRVAFIYDDDHGKHLQFSDLNMHDKEFRTYSRQASIAADSSVLIPVP
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RLLMYTESQSGYTVKEMRIDYLGETSIADSINYIDNGVVFVGSRLGDSQLIRLM
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LASVDLAGVVGIFPIRLDSNADNYVIVSLSDETHVLQITGEELEDVKLLEINTDLPTI
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SLSSSAYRDCLVISDGNSMVFGTVDDIQKIHVRSIPMGESVLRIAYQKSTSTYGVCSN
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19006. .19330,19820. .20021,20066. .20354,20814. .20956,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="M18.2"
complement(11182. .11457)
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caenorhabditis.

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,

Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,

Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,

Fulton,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,

Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,

Callaghan,M., Parsons,J., Percy,C., Rifken,L., Sonnhammer, E.,

Staden,R., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,

Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,

Vaughan,K., Waterston,R., Waterston,A., Weinstock,L.,

Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                   VESILDMDRSVAMDILSKVSDKGWDPSLPRDPVEILKVIEDLARMH"
121344. 12724
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join(21334. 121559,21610. 21835,21883. 22236,22484. 22724)
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24381. 24556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anotes "similar to RNA recognition motif. (aka RRW, RBD, or RNP domain); CDNA EST EMBL:100319 comes from this gene; CDNA EST EMBL:100219 comes from this gene; CDNA EST EMBL:100220 comes from this gene; CDNA EST EMBL:101899 comes from this gene; CDNA EST EMBL:00210 comes from this gene; CDNA EST EMBL:00210 comes from this gene; CDNA EST EMBL:002966 comes from this gene; CDNA EST EMBL:002966 comes from this gene; CDNA EST EMBL:002973 comes from this gene; CDNA EST EMBL:075932
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MLGDDTVRQAKDRGLTYFSYFAAKHIFSNRLTEYSLLKEDSANGRIVAALKYAWIIIQ
CSRCHEHLGWEYISWTREPRRFFGIQREGITFQNELQEGDTEENWDHVPPEFDNDDQEE
RTESKAERVFASKNALVTSQSRPKVASTRADMDESPPNTTSSFMVLDQNTFQVLHSHE
FGPWETALSCISGQFTNDSSTYYVVGTGLIYPDETETKIGRIVVPEVDDVERSKLRRV
HELVVRGSPLAIRILNGKLVAAINSSIRLFEWTTDKELRLECSSFNHVIALDLKVMNE
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                                                                                          EVAVADVMRSVSILSYRMLEGIRFEFVAKDMNSQWMYTCEFITAESILGGEAHLNLFTV
EVDKTRPITDDGRYVLEPTGYMVLGELPKVMTRSTLV1QPEDSI1QYSQPIMFGTNQG
TIGMIVQIDDKWKKFLIAIEKAIADSVKNCMHIEHSSYRTFVFQKRAEPPSGFVDGDL
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Caenorhabditis elegans
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U41543
U41543.1 GI:1695234
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23271. .24556
/gene="M18.7"
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DEFINITION
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ORGANISM
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CELF46H5/C
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MEDLINE
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complement(join(8345. .8450,8498. .8586,8630. .8789,
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//DA. xref="GI:1109880" ABB 17023.1."

//LTAINSLATION="MKPADGKRAFVKKRSKVTASEVRKHVISGLHPIHRLSEGDNGLD LAVSWMEXIGFTERVYDRVEVTIRR ODGLTDHNYTTIPNIENTERPOLLOGRYCLDEN SERSENSENFERPRENSENETTIR ODGLTDHNYTTIPNIENTERPOLENES STONIOPRESCHONG AND SENGRE KRAIDKNTLY SMLSKNRVKHFNNCINEERSWWENTEROPET PRILFVKVATERADPF FEPLF ASMAIYOTKNROKYTERSPAFFAN FALADHPKLDMIGSHOPNEINWENGVLENYTGKLEDMYT.

VVKIENYLOGNEVERSEPTTGTR DENNMERLERAAEN KOORLGANTSPLEGOVIDLO RIYKANYSTGASSFDRRTDPMMSQCTTASGANLTTAGGSODDGCS ITSADRISA BANGSTGAAT TARRESSEP
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/ Gene="FR6H5.4"

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PLIQDXHNGFAPDAKOPNTDLGEGKTSALVDLDPEGKFINSTRIRCGRSLQGYPFNPC
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AANACRYWPKGRGIFHNNQKTFLIWCNEEDHLRIISWOEGGWVGOVLERLIKGVKTIE
KQAPFSKDORLGWTFFCPSNLGTTVRASVHTRLPKISAKPDFKSICDGLKLQIRGIHG
ENESSEGGYVDISWKARLGLTEFEAVKQMYDGIAHLIALEKAA"
COMPLement (8345 . 12126)
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/ DEOLE 11.1109879"

/ Translation="MADYATKIPDANWVRLEIEPVOVSHDODATLNFATVQSVVPGAH
GLYXRDDGERAOLFEDNNTGXVYPPPNGWDSVPIFIHLAHGSRHGTHFADYSKANDAF
EKNISAVQKLFRAAGLGGRSQKVYAAGKTRARSTSKKNQPRGGFBAQPENVNISEESE
GRDSEKEKNDRQLEKLRNRNDELKIRVKEYKSDLSAAGLKVRNLEKKLESAQSADSEE
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AKDKUTELENOLNSDAUEETKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNODELTKEFERNELTEREKNENTERTEKSKLEWRLCELTSOWWYANE WWIDARKVÜGLESSVALGANLETANSKIGSLNODGHSSTWITTPIDGFTISGSNOGTWINDENGSSONDETTKEFERNOPETTFGALBEIPLVSALEDFAGANFFIRGGANEGRNYTLITISMTEGEVYLTGSFINWKCTLKKCEKLVSGKKGYTVNLTRGRHEFRFMINGEWATSSDYQOVPNGLGGON
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NSERVIHEAMEIPIYQASLNKSYKNVIFVYPKHINLSNRTGNARNIMIKIELMDANET
AQEVVFENGSTRMSFLTSAKTSVIYHNRTPHFIDEIKLSLPCDLNDGHHLLFTVYHIS
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VDNHKPIFSCSTEVISSVHAQDEFLENFLAGVASLSSNDPRKPPVGETQLIRSLEGLC
KTEPKKLIAFIHFIMSRLLFLIANPPYSDELSMKAFEYIGELKLFSNVLHLDLDAHQ
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KNIRLHECLLEVWLRARGSLRDVSLVHSWFLLEIILKSCSBYLTMTGRIHSPRKSRFE
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1. 38886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by sequence from more than one subclone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinton Hall Cambridge CBIO IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-NOV-1996)
On Nov 29, 1996 this sequence version replaced gi:1109877
Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans"
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                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-NOV-1995) Robert Waterston
4 (bases 1 to 38886)
Waterston.R.
The sequence of C. elegans cosmid F46H5 Unpublished (1996)
3 (bases I to 38886)
Waterston, R.
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="X"
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Db 16210 ATAATTTTGAGATAATTA 16193
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MATYSLYHFLRENFKLYRNLTRARTPLSTALSTILSSGSCGIDFVNDFERIRSLEIAN
QLAABLET PELAAKKLTEQMQELTANLQKIMLSTVRMEHUNDYEMTIOLMYQLVEG
YSNNPDLRTWALLNARERHEKQRNLCEAAHSYLQASALVFEYTAQKONLSFESKGAA
TFSEITPNAIKESKTNFNSLKNADSENHIQSYHTEAGVIKILEKAFALLEKAQLYEL
                                                           LOSHDLDDRIVEGESLAQVANIYKPLYTIVLDNIECLHSGSVRNSTDVSSTNSFVEQT
ORODVMAAIAGKLRNSPDPTFGKQQMDLPMTKTILCCVFWVLRNIDREDLKHWIRSLD
NENMLKMLHILFHTMTSFEIKDDPASARRSPDKTSLTKLDEEPEPGQVKWRAQSSETC
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RCEGSFFRVAFYGKLFGALNNAEFVYKESAFSKLNEISNRLETFYTNMYGEGNVVVLK
DSKPVQLEKLNPEKAYIO1TFVDVYLSDNEKMERTTYFTRNNVNRFYFEAPYTMEGR
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/gene="F46H5.5"
/gene="F46H5.5"
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25768. .26131,25185. .25312)
/gene="F46H5.5"
/codo__start=1
/evidence=not_experimental
/protein_id="AAB37026.1"
EOFLKNLETLVDILAQEVIIRHTNDPDKARNISNSIGYFLRDCFSIMDRTFVMKLVHK
YLIAFAESMRKLVHSNELLSIKIDEVVVVCSTSETYIIVNILSDLKRSGATNGGAVPPA
SFLSGNRYKSSELTSWTLNDISRSTHYLSGQVLSDMRDSIISGKTTLCARAIETVKEL
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AQHKNPKMLSMFIQGSIGTTVNQGPLEIANVFLANAMLDDRGRPVDRLQNKLRLSFRH
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Submitted (03-AdG-1999) Production Sequencing Facility, DOE Joint Submitted (03-AdG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA *Www.jgi.doe.gov.

* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.
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1684: contig of 841 bp in length
gap of unknown length
2545: contig of 861 bp in length
gap of unknown length
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PROGRESS ***, 31 unordered pieces.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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KEYWORDS

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AC012518 57784 bp DNA HTG 30-OCT-1999
Homo sapiens clone RP11-512G13, *** SEQUENCING IN PROGRESS ***,
unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 57784)

Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Boate, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
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/ Organisma-"Homo sapiens"
/ db.xref="taxon:9606"
/chromosome="5"
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S DOE Joint Genome Institute.

Direct Submission

Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Malint Creek, CA 94598, USA

* NOTE: This is a 'working draft' sequence. It currently

* consists of 40 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                          AC016648 45617 bp DNA HTG 04-DEC-1999
Homo sapiens chromosome 5 clone RPCI-1_137K24, *** SEQUENCING IN
PROGRESS ***, 40 unordered pieces.
                                                                                                                                                                                 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 45617)

DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: contig of lut.
gap of unknown length
77: contig of 735 bp in length
gap of unknown length
698: contig of 921 bp in length
gap of unknown length
- nntig of 719 bp in length
- nntig of 719 bp in length
- length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f unknown length
9 of 1043 bp in length
f unknown length
9 of 1310 bp in length
f unknown length
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                          RESULT 40
AC016648/c
LOCUS
DEFINITION
                                                                                                               ACCESSION
VERSION
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RESULT 42
ACO10280/C
LOCUS
ACO10280 70390 bp DNA
DEFINITION Homo sapiens chromosome 5 clone CIT-HSPC_537E7, *** SEQUENCING IN
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Pred. No. 42;
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martinez, C., McLedd, M.P., Mei, G., Morgan, M., Morris, S., Marinez, C., McLedd, M.P., Mei, G., Morgan, M., Morris, S., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Ouiles, M., Reliect, D., Rives, M., Samuel, S., Scherrer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, G., Weinstock, G., Weinston, R., Wolliamson, A., Worley, K., Wren, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

Submitted (29-GCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

** NOTE: This is a "working draft" sequence. It currently

** consists of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2: contig of 1419 bp in length
3: contig of 1388 bp in length
7: contig of 1388 bp in length
17: gap of unknown length
11: contig of 1374 bp in length
11: contig of 1374 bp in length
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gap of unknown length
contig of 2165 bp in length
gap of unknown length
contig of 2149 bp in length
gap of unknown length
gap of unknown length
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of 1270 bp in l
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of 1506
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COMMENT

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Dipublished

Chases I to 71293)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Howland, J., Johnson, R., Jones, C., Rann, L., Raratas, A., Klein, J., Howland, J., Lieu, C., Locke, K., MacGonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Melterson, K., Pollara, V., Rilley, R., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasailiev, H., Vo, A., Wheeler, J., Wu, X., Wwman, D., Ye, W. J. Zimmer, A. and Zody, M., Andeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M., Andeler, J., Wu, X., Direct Submission, A., Lander, A., and Zody, M., A., Wasailiev, R., McK., McK
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                 Direct Submission
Submitted (24-FEB-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC016217 71293 bp DNA HTG 23-NOV-1999
Homo sapiens clone RP11-26F18, LOW-PASS SEQUENCE SAMPLING.
AC016217
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 71293)
                                                                                                                               Structural Analysis of Arabidopsis thaliana Chromosome 3. Unpublished (1998)
2 (bases 1 to 70952)
Nakamura, Y.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Columbia"
/db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .70952
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                                                                       Arabidopsis
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Nakamura, Y.
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AB024028
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contig of 1022 bp in length
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Mismatches

    70390
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    /db_xref="taxon:9606"
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Pred. No.
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* 23519 24371: contig of 853 bp in length * 24372 25255: contig of 864 bp in length * 24372 25255: contig of 884 bp in length * 25256 26130: contig of 875 bp in length * 26131 27011: contig of 875 bp in length * 26131 27011: contig of 881 bp in length		* 31419 32331: contig of 913 bp in length * 32332 33232: contig of 901 bp in length * 33233 34112: contig of 80 bp in length * 33233 34112: contig of 80 bp in length * 34113 35013: contig of 901 bp in length * 34113 35013: contig of 901 bp in length * 35014 35911: contig of 898 bp in length		41212: contrig 42096: contrig 42096: contrig 42972: contrig 43868: contrig 44749: contrig 9ap of 45637: contrig	
Center: Whitehead Institute/ MIT Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submission@genome.wi.mit.edu Contact: sequence_submission@genome.wi.mit.edu Center project Information Center project name: L4628 Center clone name: 26 F_18	T S S S A C L D T B S	be preserved. 845: contig of 845 bp in length gap of unknown length 846 1716: contig of 871 bp in length gap of unknown length 1717 2589: contig of 873 bp in length gap of unknown length	7 4294: contig of 8 2 gap of unkn 5 5182: contig of 8 6077: contig of 8 6075: contig of 8 6955: contig of 8 6955: contig of 8 7812: contig of 8 940 of unkn 6 7812: contig of 8		UNK BOOK BOOK BOOK BOOK BOOK BOOK BOOK BO

33663388 /note="(CAAAA)n"	/rpt_tamily="Simple_repeat" 4271. 4750 /note='MZEF"	/evidence-not_experimental complement(43784937)	/note="GENSCAN" complement(4397, .4422)	/uote= Aroons /evidence=not_experimental 44684490	/note="XPOUND" /evidence=not_experimental	44974314 /note="xPoUND" /evidence=not_experimental complement(51715319)	/rpt_family="MIR" 5471.5638	/uote=ware /evidence=not_experimental complement(58595901) /note=war_rich"	<pre>// Type_rammily= Low_complexity 59756002 //note="AT_rich" //rpt_family="Low_complexity" //rpt_family="Low_complexity" //rpt_family="Low_complexity"</pre>	/rpt_family="Alusx" complement(78917933)	/note="(TAGA)n" /rpt_family="Simple_repeat" 80608121	/rpt_ramliy="Mullu" complement(88238905) /note="MarEr" /avidancemont evnerimental	/evidence.not_ckpci.mcn.dr //oote="AI_rich" //oote="AI_rich"	/rpt_ramily="Low_complexity" complement(963210675) /rpt_family="LiMC1" 10002 1034		/rpt_complement(13170. 13373)	/rpt_family="MLT2B" complement(1331913358)	/ucce=not_experimental 1337414061	/rpt_family="L1ME1" 1407014283	/rpt_family="L1MEc_5end" 1417714234	/noce="Makk" /ovidence=not_experimental 1531315404	/note="GRAIL" /note="GRAIL" /coldence=not_experimental	1031310404 /note="MZEF" /avidence=not experimental	complement(1609716540) /rpt_family="LIMEa_5end"	1656018253 /rpt_family="L1M2_orf2"	complement(17b1/1/810) /rpt_family="MER30" complement(1763517698)
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56211: contig of 880 gap of unknow	of 866 unknow	57964 58866: contig	gap of unknow 58867 59738: contig of 872	<pre>* s9739 60635: contig of 897 bp in length * s9739 60635 contig of 897 bp in length * gap of unknown length</pre>	60636 61519: contig of 884 gap of unknow	* 61520 62425: contig of 906 bp in length * 62426 63299: contig of 874 bp in length	gap of unknown 63300 64178: contig of 879 gap of unknown	Query Match 9.1%; Score 18; DB 44; Length 71293; Best Local Similarity 100.0%; Pred. No. 41; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 149 AGCATTTACAAGAACAAG 166 	7 W. T.		AF191071 AF191071.1 GI:6018318 HTG.	SOURCE numan. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 88481) AUTHORS Reichwald, K., Baumgart, C., Dette, M., Menzel, U., Schillhabel, M.,	Weng, G. and Rosenthal, A. TITLE Direct Submission JOURNAL Submitted (29-SEP-1999) Genome Analysis, Institute of Molecular	Biotechnology, Beutenbergstrasse II, Jena U/45, Germany Location/Qualifiers FEATURES 1 RARA1	/organism="Homo sapiens" /db_xref="taxon:9606"	/Chromosome="8" /clone="BAC 388D06" repeat region 172	/rpt_family="Ll 681499	75 /15 /15 /15 /15 /15 /15 /15 /15 /15 /1	/note="GRAIL" /evidence=not_experimental renest region 1352 2244	exon 1851. 2027		repeat_region 22562504 /rpt_family="AluSp" reneat region 2789 .2811		repeat_region 28802932 /note="AT_rich" /rpt_family="Low_complexity"

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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HS398C22
AC002126
AC009012
HSJ506G21
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AC006563
AC008020
AC010104
AB024745
AC05214
HS403M6
HS135E14
AC005951
AC005951
AC005951
AC005951
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AC007158
HUMVIPHM1
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AC008821
AC002120
U73643
AC014889
HSS06G2B
AC000394
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AC011108
AB026647
HS931E15
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AC013370
HS262D12
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                                               (without alignments)
-43.875 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AL049761 Human DNA 285987 Human DNA s Continuation (3 of AC015845 Homo sapi Continuation (3 of AC013673 Homo sapi

112K5

ALIGNMENTS

AC003071 Homo sapi AC017236 Drosophil AC002466 Human BAC AC003062 Mouse Chr AC010025 Drosophil AC010143 Homo sapi AC008020 Mus muscu AC008020 Mus muscu AC010104 Homo sapi

Description

SUMMARIES

2

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9974. .10119,11527. .12931,14076. .14186,14656. .14744,
17677. .17848)
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LOWLDCVHQLQRQFPCSFEFNEAFLVKLVQHTYSCLFGTFLCNNAKERGEKHTQERTC
SVWSLLRAGNKAFKNLLYSSQSEAVLYPVCHVRNLMLWSAVYLPCPSPTTPVDDSCAP
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SIRLLCTQMPDPGNWLSALESTKWLHHLSVLLKSALLVVHAVDQDQRPVLVHCSDGWD
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5401. .5577
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4415. .4611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-NOV-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 150228)
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Submitted (18-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY: WUGSC
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NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is DJ0394A18, 200 bp overlap; the
clone sequenced to the right is DJ43804, 200 bp overlap. Actual
start of this clone is at base position 1 of BK085E05.
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15028)
Sulston,J.E. and Waterston,R.
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Bradshaw, H., Graves, T., Sutterer, C. and Ozersky, P.
The sequence of Homo sapiens BAC clone BK085E05
Thomboblished (1999)
3 (bases 1 to 150228)
Waterston, R.
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/db_xref="taxon:9606"
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/clone="BK085E05"
<19. .17848
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
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     GI:2588643
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Submitted (20-AUG-1997) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA SUBMITTED BY Generics Center Department of Genetics Washington University St. Louis MO 63108, USA St. Louis MO 63108, USA Mustl.edu/gsc mailto:saplens@watson.wustl.edu/gsc
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                                                                                   Discophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 22287)

S Adams, M. and Venter, J.C.

Direct Submission

L Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, ODEC-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, ODEC-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, Working draft's sequence.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 78154)
Miller,N and Gibson,A.
The sequence of H. sapiens BAC clone RG354L07
Unpublished (1997)

Z (bases 1 to 78154)
Waterston,R.
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Human BAC clone RG354L07 from 7q31, complete sequence.
AC002466
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/db_xref="taxon:7227"
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Pred. No. 0.41;
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
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                                                                                                                                                                                                                                           /note="similar to EST AA230681 (NID:g1852980) mv76a09.rl"
14655. 14745
/gene="wuGsC:H_BK085E05.l"
complement(14682. 14745)
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/note="match to EST AA508154 (NID:g2244593) ng93g05.sl"
15909. 15939
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1775. .18059
/note="match to EST R24323 (NID:g779211) yg32e07.rl"
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1817. .18531
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18453. .18915
/note="match to EST N39988 (NID:g1163533) yx97g05.rl"
18501. .18809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(17675. .18023)
Anote="match to EST AA508154 (NID:g2244593) ng93g05.sl"
17675. .17821
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18676. .19007
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18784. .19060
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18945. 19313

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 16074 CCACCGCACCTGGCTGATGCTTTTCTATCTGACTTCTTTCAGAGGACCCTGAAAGACACT 16015
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/note="match to EST N26968 (NID:91141316) yx18f03.rl"
complement(19287. .19546)
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10595...1269

/rptc_family="Alu"

12297...12773

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12430...12694
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12831. .12935
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                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="POLY_A"
16061. 16367
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/rpt_family="Alu"
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Matches 137; Conservative
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100.0%; Pred. No. 0.4;
tive 0; Mismatches 0
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complement(73916. .74206)
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complement(75596. .76628)
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a 13876 c 14122 g 24787 t
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                                                                                                                                                                                                                                                                                                                                                                                              40560. .40854
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complement(60918.
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complement(35485.
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4718. .34737
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Best Local Similarity 100.
Matches 20; Conservative
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                                                             The sequence of this clone was established as part of a mapping and sequencing collaboration between the NiGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/lik/GIB/CHR7 or send mailto:egreen@nhgri.nih.gov
                                                                                                                                                                                                                              This clone is from a release of the human BAC library. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 84:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RG354L07;
actual end is at 78154 of RG354L07. The orientation of this clone
is unknown.
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sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4625. .4923)
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/rpt_family="L1"
/rpt_family="L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MER"
complement(7430, 7453)
/rpt_family="ME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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1985, .2017
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4112. .14318
                                                 MAPPING INFORMATION
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Gaps

DEFINITION RESULT 4 AC003062/c

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

JOURNAL REFERENCE

AUTHORS

REFERENCE AUTHORS

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LIGHT IN.

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EURATYOLA; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

PLETYGOTA; Neoptera; Endoptera; Drosophila.

PLETYGOTA; Neoptera; Endoptera; Drosophila.

1 (bases 1 to 149625)

SS Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

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Couvara, W., Harrias, K., Hernandez, J., Hodgson, L., Hodgson, M.,

Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jai, Y., Jones, M.,

Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,

Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lu, W., Logan, N., Morris, S.,

Nash, S., Nelson, A., Payton, B., Perez, L., Pu, L.L., Quiles, M.,

Reiter, D., Rives, M., Samuel, S., Sap, J., Scherer, S., Shah, E.,

Shen, H., Shmon, M., Sparks, A., Stamps, A., Scherer, S., Shah, E.,

Reinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J.,

Nenstock, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R.,

Direct Submission
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Submitted (11-SEP-1999) Human Genome Sequencing Center, Department
Submitted (11-SEP-1999) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 16, 1999 this sequence version replaced gi:5916438.
* NOTE: This is a "working draft' sequence. It currently
* Consists of 57 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                        AC010025 149625 bp DNA HTG 16-OCT-1999 Drosophila melanogaster chromosome 3L/69D4 clone RPC198-20B1, SEQUENCING IN PROGRESS ***, 57 unordered pieces.
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Unpublished 2 (bases 1 to 149625) Worley, K.C.
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AC010025.4 GI:6056162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-SEP-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval Room 208, Norman, OK 73019, USA
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Submitted (23-SEP-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-NOV-1997) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
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Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
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Galili,N., Baldwin,S., Lund,J., Reeves,R., Gong,W., Chen,F.,
Roe,B.A., Emanuel,B.S., Nayak,S., Mickanin,C., Budarf,M.L. and
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 89743)
Chen,F. and Roe,B.A.
                                                                                                                                                                            AC003062 89743 bp DNA ROD 03-MAY-1999
Mouse Chromosome 16 Region Syntenic to DGCR BAC Clone b264n1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Region of Mouse Chromosome 16 is Syntenic to the DiGeorge, Velo-Cardio-Facial Syndrome Minimal Critical Region Unpublished
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/db_xref="taxon:10090"
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1. .89743
      Db 75221 TCCAAGCTAAAACAATTCTC 75240
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Roe, B.A. Dr.
Direct Submission
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4 (bases 1 to 89743)
Roe, B.A. Dr.
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Roe, B.A. Dr.
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6 (bases 1 to 89743)
Roe,B.A. Dr.
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Matches 20; Conserv
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FEATURES

COMMENT

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Waterston, R. H.

Direct Submission

Submitted (13-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
MO 63108, USA

On Sep 21, 1999 this sequence version replaced gi:5870891.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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1 (bases 1 to 177591)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Boyle, C.M., Farfan, D.E., Hummasti, S.R., Harris, N.L., Hoskins, R.A., Harris, N.L., Hoskins, R.A., Houston, R.A., Hummasti, S.R., Rarra, R., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sequeira, A., Sequeira, S. Shi, H., Sair, E., and Syriskas, R.R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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2. (bases 1 to 177591)
4. (bases 1 to 177591)
5. (charlet, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Boyle, C.M., Farfan, D.E., Galle, R., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Macda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
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0.39;
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/db_xref="taxon:9606"
/clone="NH0301017"
47710 a 37779 c 38757 g 49763
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Homo sapiens clone NH0301017, *** SEQUENCING IN PROGRESS ***, 4
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174063)
Waterston, R.H.
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/db_xref="taxon:7227"
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/clone="RPC198-20B1"
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                                                                                The sequence of Homo sapiens clone Unpublished
   138 2510; contig of III
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COMMENT

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Deschamps, S., Comen, S. and Roe, B.A.

Direct Submission

Lisubmitted (10-UUL-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

ON NOV 21, 1999 this sequence version replaced gi:6403511.

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
180513 bp DNA HTG 23-NOV-1999
is, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.
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HOMO Sapiens clone NH0540C18, *** SEQUENCING IN PROGRESS ***, 2
unordered pieces.
AC010104
AC010104.2 GI:6136424
HTG; HTGS_PHASE1.
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 180513) Deschamps, S., Oomen, S., Darber, R., Becat, C. and Roe, B.A. Mus musculus Chromosome 16 PAC Clone p598k13
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80446: contig of 7275 bp in length
80512: gap of unknown length
111027: contig of 30515 bp in length
111093: gap of unknown length
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of 42105 bp in length.
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/db_xref="taxon:10090"
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                                                                               Laboratory, MS 64-121, Berkeley, CA 94720, USA
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Aug 2, 1999 this sequence version replaced 91:5630021.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web Site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
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    Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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Drosophila melanogaster BAC library, partial EcoRI in
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68720: gap of unknown length
95333: contig of 26613 bp in length
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177591: contig of 210 bp in length
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/chromosome="3"
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                                            Rubin, G.M.
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FEATURES

BASE COUNT

RESULT AC008020

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YYWHYDSGSTOWQRPTWELGOAEDPGTGTEGIWGLRPPKGRSFSSLESSLDRSNSLSW
YGESY 102NEPGARCFAVRSLGWYEVPEEDLAPGKSSIAVNNCIQOLAQTRSRSOPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC005214 50511 bp DNA PRI 01-JUL-1998
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete
                                                                     1105. 6764

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join(1105. 1153,1435. 1598,1680. .1756,2626. .2686,

2850. .2996,3122. 3249,3500. .3505,3648. .3762,3900.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50511)

Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M., Sequencing of human chromosome 5

Chases 1 to 50511)

Ricke, D.D.

Ricke, D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A. Sequence submitted by:

DOE Joint Genome Institute.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
Direct Submission
                                                                                                                                                                                                            /function="interacting with Alzheimer's beta-amyloid precursor protein"
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1105. .6764
    .018
note="transcription start site"
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                  Louis,
                                                                                                                                                                                Direct Submission
Submitted (11-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Lou University School of Medicine, 4444 Forest Park Parkway, St. Lou MO 63108, USA
On Oct 27, 1999 this sequence version replaced gi:5870287.
* NOTE: This is a "working draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 189870)
Waterston, R. H.
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                                                                                               The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 189870)
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Fanahashi,H. and Tabira,T.
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Tanahashi, H.
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Homo sapiens
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Gaps

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omplement'17
                                                                                                                 .14712)
                                      .13195)
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12966. 13101
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13411. 13716
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14850. 14873
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complement(16233.
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             repeat_region
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complement(11455. .11800)

/note="82% identity mouse EST ud02f04.rl"

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/standard_name="zk35d07"

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complement(12811. .12965)
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56. 1239
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7100. 2142
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2662. 2748
note="GRAIL 2 excellent exon, frame 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              omplement(8225. .8324)
note="GRAIL 2 excellent exon, frame 0"
                                                                                                                                                                                                  frame 2"
                                                                                                                                                                                         859. 2937
note="GRAIL 2 excellent exon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L1"
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749. 5994
/note="Alusx repeat: matches 5. 251 of consensus"
6140. 643.
/note="Alusx repeat: matches 1. 305 of consensus"
6443. 6748
/note="Alusx repeat: matches 1. 297 of consensus"
6780. 6877
/note="Alusp/q repeat: matches 215. 312 of consensus"
7006. 7288
/note="Alusp repeat: matches 1. 291 of consensus"
7289. 7765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"LiPal6 repeat: matches 5804. .5943 of consensus" 3673. .3960
/note-"Alusx repeat: matches 1. .305 of consensus" 3961. .3982
/note-"11 copies 2 mer tg 100% conserved" 4022. .4061
/note-"20 copies 2 mer at 80% conserved" 4037. .4379
                                                                                                                                                                                                                                                                                                                                                                                                     .091. .2330
/note="LIPA16 repeat: matches 5943. .6157 of consensus"
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4097. .4379
/note="AluSx repeat: matches 1. .282 of consensus"
n 4434. .4545
/note="56 copies 2 mer at 83% conserved"
1 4546. .4579
/note="17 copies 2 mer ac 100% conserved"
1 4605. .4910
/note="Alubr repeat: matches 1. .307 of consensus"
5749. 5994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alux repeat: matches 167. .307 of consensus"
13166. 13471
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1056. .10343
/note="LiMB1 repeat: matches 6099. .6173 of consens
10456. .10841
/note="match: GSS AQ134006"
                                                                                                                                                                                                                                                                                                                       1672. 1982
/note="AluSx repeat: matches 1. .312 of consensus"
2091. .2330
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13662. .13977
                                                                                                                                                                                                                                                                                                                                                                                                                                        2331. .2630
/note="Alusg repeat: matches 1. .300 of consensus"
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/note="AluSx repeat: matches 5. .300 of consensus"
9904. .10199
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7870. .8149
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                   /map="q24.1-25.2"
/clone="RP3-403M6"
/clone_lib="RPCI-3"
201. .494
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                                                  FEATURES
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Submitted (20-MAY-1999) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. Email enquiries: humquery@sanger.ac.uk Clone
requests: clonereques@sanger.ac.uk

On May 13, 1999 this sequence version replaced gi:4678468.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL: Sw:, SWISSPROT: Tr:, TREMBL
This sequence is the entire insert of clone 403M6. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
complement(27838. .27936)
/note="GRNIL 2 excellent exon, frame 0"
join(29553. .29612,29893. .30060,30138. .30215,31580. .31709,
32097. .33224,32706. .32798,33054. .33177,33302. .33498,
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403M6 is from the library RPCI3 constructed at the Roswell Park
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86329)
Williams, S.
                                                                                                       /standard_name="Fe65L2"
/note="80%-91% identity rat Y13413 transcriptional
activator FE65"
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                                                                                                                                                                                  Complement (30471, .30874)
/rpt_damily="Alu"
31341. .31456
/note="GRAIL 2 excellent exon, frame 1"
31582. .31709
/note="GRAIL 2 excellent exon, frame 0"
32108 ..32222.
                                                                                                                                                                                                                                                                                                                                                                                      32684. 32791
/note="RAIL 2 excellent exon, frame 0"
33055. 33206
/note="RAIL 2 excellent exon, frame 2"
34605. 34751
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Pred. No.
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        Qy
        111 GATCACCTCTGTTCAGTCC 129

        Db
        31223 GATCACCTCTGTTCAGTCC 31205

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Best Local Similarity 100.4
Matches 19; Conservative
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VERSION
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AUTHORS
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JOURNAL
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COMMENT

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/note="LiMBB repeat: matches 5840. .6173 of consensus" 15090. .15391
/note="AlluSp repeat: matches 1. .303 of consensus" 15392. .15828
/note="LiMBB repeat: matches 5386. .5840 of consensus" 15461. .15904
/note="match: EST M62284" 16184. .16358
/note="LiMC4 repeat: matches 7705. .7880 of consensus" 16184. .1659
/note="AlluSx repeat: matches 1. .298 of consensus" 16699. .1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Lind" repeat: matches 7370. .7413 of consensus" 18786. .1908
/note="Alusg repeat: matches 5. .301 of consensus" 19108. .19412
/note="Alusg repeat: matches 1. .298 of consensus" 19857. .20147
/note="Alusb repeat: matches 3. .292 of consensus" 22576. .22624
/note="L2 repeat: matches 2701. .2749 of consensus" 22979. .23014
/note="L2 repeat: matches 2701. .2749 of consensus" 22979. .23014
/note="L2 repeat: matches 2701. .2749 of consensus" 22978. .23014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSx repeat: matches 1. .304 of consensus"
17093. .17402
/note="AluJo repeat: matches 1. .306 of consensus"
/note="MulJo repeat: matches 1. .306 of consensus"
complement(17391. .1762)
/note="match: STS G08536 G09147"
17528. .17865
/note="12 copies 2 mer ga 76% conserved"
17572. .17865
/note="Mulsx repeat: matches 1. .282 of consensus"
17866. .17957
/note="LJMC4 repeat: matches 7413. .7505 of consensus"
17958. .18240
/note="AluYb& repeat: matches 1. .298 of consensus"
18241. .18284
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Anote="Aluyb repeat: matches 1. .307 of consensus" 30419. .30452
Anote="7 copies 2 mer tg 100% conserved" 319467. .31194
Anote="Aluxg repeat: matches 18. .298 of consensus" 31963. .32272
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24736. .24898
/note="FRAM repeat: matches 5. .161 of consensus"
25209. .25316
/note="LiME repeat: matches 5683. .5790 of consensus"
25549. .25646
/note="U6 repeat: matches 1. .107 of consensus"
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Note="FRAM repeat: matches 0. .175 of consensus"

86174. .27021

Note="AluJo repeat: matches 11. .305 of consensus"

27122. .27443
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83708. .23999
matches 1. .307 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //octe="Aluy repeat: matches 1. .309 of consensus"
            note="AluSg repeat: 3978. .14013
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PAC RPCIP704E14135Q2, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Max-Planck-Institut fuer Molekulare Genetik
Innestrass 73, D-14195 Berlin-Dahlem, Germany
All annotations in this database entry are developed by
computational tools. It is therefore not explicitly noted in the
feature lines that evidence is not experimental.
PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135855)
Brandt,P., Dose,S., Grimm,M., Groet,J., Hornischer,K.,
Loehnert,T.H., Nizetic,D., Scharfe,M., Schoen,O., Yaspo,M.L. and
              /note="Alujo repeat: matches 1. .312 of consensus" 32627 .33244
/note="LipA7 repeat: matches 5520. .6138 of consensus" 3267 .33567 .33567 .33567 .33567 .3357 .3357 .3357 .335194)
/note="Malusgi repeat: matches 1. .301 of consensus" complement(34525 .35194)
/note="match: GSS AQ268889" complement(34670 .35222)
/note="match: GSS AQ353171" 35217 .35639
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                   /note="match: GSSs AQ200990 AQ505480"
55640. 35943
/note="AluSp repeat: matches 1. .300 of consensus"
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'AnnoMitter' (Hornischer & Bloecker).
Programs used by 'AnnoMitter':
                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 11; Length 86329;
Pred. No. 1.5;
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Mascheroder Weg 1, D-38124 Braunschweig, Germany,
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. Used matrix: vertebrate: Minimum score:
> Grail (Xu et al.), Vers. 1.3
> Organism: human
> Mzef (Zhang)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center for applied Molecular Biology
School of Pharmacy, University of London
29-39 Brunschwig Square, London, WClN lAX,
e.mall: j.groet@chemb.ulsop.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence overlaps with Acc.Nr. AJ010597 Collaborators:
                                                                                                                                                                                                                                                                                                                                                      13.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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. Organism: human
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Homo sapiens chromosome AJ010598
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Best Local Similarity 100.
Matches 19; Conservative
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//note="GENSCAN prediction, score = 4.94; GRAIL, score = 100%, comment = excellent; MZEF prediction, score = 0.666"
100%, comment = excellent; MZEF prediction, score = 0.666"
100%, comment = excellent; MZEF prediction, score = 0.666"

/note="Insertion in AJ010597, pos. 95684. 95686"
/replace="tte."
/repla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum score: 60; Minimum identity, 'v.',

'Tandem Repeats': 20 potion 'tandem'
Minimum length 2 bp: Maximum length 20 bp: Score threshold 20.

Treat N's as mismatches? YES; Allow uniform consens? NO >

'Inverted Repeats': GDE 2.2 option 'inverted'
> 'Micro Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands': GDE 2.2 option 'opg'
. CpG island region size 100 bp:
. Minimum GC contents 50 %; Observed/Expected 0.6 > 'STS Scan':
e-PCR (Schuler)
Margin: 50; Number of mismatches allowed: 0; Word size: 7 .

STS database: AbSTS markers'
> 'ERNA Scan': tRNAscan-SE (Lowe & Eddy), Vers. 1.11.
probability: 0.04; Overlapping number: 0 > Xpound (Thomas
                                                                 Base score cutoff: 0.2; Minimal exon length: 3 bp > 'Repeats': BLASTN 2.0.9 (Altschul et al.)

Database(s): *RepBase (Human), released 22-DEC-1995 .

*RepBase (mammal), released 22-DEC-1995 . Minimum identity: 70 %;

> 'ESTS': BLASTN 2.0.9 (Altschul et al.)

Database(s): * embl (EST), Vers. 60 (16-SEP-1999) . Using unmasked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Using unmasked
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/note="match: ESTS AW051819 H72628 AI608668 AI032875
AA181987 AA486559 AA244397 AI669239 AL043105 H49262
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> 'GSSs': BLASTN 2.0.9 (Altschul et al.)
Database(s): * embl (GSS), Vers. 60 (16-SEP-1999) 
* emblnew (GSS), Vers. 60+ (20-OCT-1999) . Using
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"match: EST AA482201"
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/map="21q11.2"
1. .12050
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/db_xref="taxon:9606"
/chromosome="21"
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1. 135855
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/note="AGC repeat"
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R16068 AL073993 AL727192 AL56252 H61034 AL051619 H79348
A1473949 AA878105 AL832910 AA483936 AL083610 AA745538
A310556 AL035988 AA385780 AL168100 AA877973 AL224602
AA878106 AA252230 AL453299 N41859 AA58242 AL953769
AA673211 A1978999 AA18674 AA569591 AA631359 AL125714
AA67321 A197899 AA18044 AA569591 AA631359 AL185714
AA67321 A197899 AL83249 AA282905 A1168101 AA682635
AA716522 AA019068 A1813494 AL038528 N57933 AA775332
AA6809926 AA487071 A168363 AA469242 C75350 T93092 AA764040
AA642464 AA70153 AA53459 AA664999 A17218 H61906 A1268826 AA999694
AA014144 AA733435 AA664999 A17218 H61906 A126826 AA999694
AA676494 AA71218 AA604999 AA669999 AA699099 AA69999 A1991954
AA526639 AA113159 AW082490 AW006930 AW069919 AW007621
AW078909 A1991293 AW0789 AL685964 AA643864"
C2552 2341): .(2311.2397)
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/note="GENSCAN prediction, score ~ 3.89; GRAIL, score ~ 1.00%, comment = excellent; MZEF prediction, score ~ 0.996" 4138. .4180
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/note="86% identity: matches 11...124 of consensus"
2782...2847
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/note="XPOUND prediction, score ~ 0.528"
3707. .3732
/note="R1, 84% complementary to IR1' (3750.
7754_type=INVERTED
3750. .3775
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/note="IR1', 84% complementary to IR1 (3707.
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/rpt_type=TANDEM

/rpt_type=TANDEM

/rpt_type=TANDEM

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4104. 4180
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complement(2842. 2965)
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3032. 3072
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/note="match: GSS AQ535294"
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/note="match: EST AI160319"
complement(3043. 3076)
/note="match: EST AA642169"
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/note="match: GSS AQ728019"
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/note="match: EST W91939"
complement(2798. .2965)
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3842. .3868
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http://ftp.genome.washington.edu/RW/RepeatMasker.html
Location/Qualifiers
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                                                                                                                    /clone="hRPK.372_K_20"
/clone_lib="RPCI-11 human BAC library"
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/rpt_family="MLTII"
complement(26155. 27023)
/rpt_family="Lip"
27025. 27424
/rpt_family="LiPal3"
28022. 28136
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(7479. 18301
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complement(15552. .17481)
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complement(13005. 13180)
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/db_xref="taxon:9606"
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complement//fence
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1963. 12.
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20135. .20462
/rpt_family="MLTIA1"
21131. .22493
/rpt_family="LIMB8"
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'rpt_family="(TAAAA)n"
.z594. .12698
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/rpt_family="LIMB8"
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!5958. .26130
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complement(19533.
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    Green, P. (1996-1997)
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20101. .20
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Direct Submission

Submitted (07-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Joses 1 to 155450)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barna, M., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cenry, J., Colangelo, M., Collins, S., Cooke, P., Corliss, D., Depayre, E., Devon, K., Brown, C., Gardjer, R., FitzHugh, W., Forrest, C., Funke, R., Gardjer, M., Gardjer, M., Gardjer, M., Gardjer, M., Mardon, S., Gardjery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., McGurk, A., McKernan, K., Maldrim, J., Molla, M., Morris, W., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Verw, J., Land, J., Waller, J., Wyman, D., Verw, J., Zho, J., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC005951 155450 bp DNA PRI 18-NOV-1998
HOMO Sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
AC005951
AC005951.1 GI:3892081
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4370. .4708

/note="match: EST H69816"

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(4786.4813). .(4836.4885)

/note="match: ESTs A1243353 A1357315 AA325371 A1338348
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. ...
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Pred. No.
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Cubmitted (16-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 157176)
Waterston, R.H.
Direct Submission
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 157176)
Waterston, R.H.
Waterston, R.H.
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Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (23-OCT-1999) Department of Genetics, Washington
Submitted (23-OCT-1999) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 23, 1999 this sequence version replaced gi:5649381.
SUBMITTED BY: WUGSC
Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 157176)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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HOMO sapiens BAC clone NH0090D01 from 2, complete sequence.
AC007092
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                                         13.9%; Score 19; DB 40; Length 155450; 100.0%; Pred. No. 1.5;
                                                                                             Indels
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The sequence of Homo sapiens BAC clone NH0090D01
Unpublished
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                                                                                           Mismatches
complement(46617. .46812)
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Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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                                                                                                                                                                  Db 52813 CCACCGCACCTGGCTGATG 52795
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Waterston, R.H.
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                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Cataneso, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                       VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is NH0179A20; the clone sequenced to the left is NH0179A20; the clone sequenced to the sequenced clone is at base position 15376 of NH0260K08.

Location/Qualifiers

1. 157176
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/db_xref="taxon:9606"
/chromosome="2"
/map="2"
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8098. 28126
8137. 28128
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/rpt_family="MIR"

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6812. .6880
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                                                SOURCE INFORMATION:
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Length 157176;

Gaps

DB 40; 1.5;

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Indels

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE JOURNAL REFERENCE AUTHORS

AUTHORS REFERENCE

RESULT 16 AC012536/c DEFINITION

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AL LUBRATE 1. COLINGARY 1998) Chromosome 6 Project Group Standary 5. Direct Submission S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS179N16 172048 bp DNA PRI 23-NOV-1999
HOMO Sapiens DNA sequence from PAC 179N16 on chromosome
62021.1-21.3. Contains the SAPK4 (MAPK p38delta) gene, and the
alternatively spliced SAPK2 gene coding for CSaids binding protein
CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two
predicted CPG islands, complete sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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gap of unknown length
): contig of 2176 bp in length
2: contig of unknown length
gap of unknown length
7: contig of 11565 bp in length
gap of unknown length
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gap of unknown length
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9: contig of 24889 bp in length
9: contig of 24889 bp in length
gap of unknown length
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of 48797 bp in length.
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Location/Qualifiers
1...160798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-11472"
51460 a 28275 c 27976 g 53079 t 8 o
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Pred. No.
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                              AC012536 160798 bp DNA HTG 30-NOV-1999
Homo sapiens clone RP11-114J22, WORKING DRAFT SEQUENCE, 9 unordered
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Submitted (29-OCT-1999) Whitehead Institute/MIT Center for Genome Submitted (29-OCT-1999) Whitehead Institute/MIT Center for Genome Seearch, 320 Charles Street, Cambridge, MA 02141, USA
On Now 30, 1999 this sequence version replaced gi:6139161.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homosapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160798)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-114J22
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Center clone name: 114_5_2

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap: version 0.960731

Consensus quality: 183554 bases at least 040

Consensus quality: 157431 bases at least 030

Consensus quality: 157431 bases at least 020

Insert size: 163000; agarose-fp

Insert size: 160798; sum-of-contigs

Quality coverage: 4.9 in 020 bases; sum-of-contigs

Quality coverage: 5.0 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
------- Project Information
Center project name: L1935
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gap of unknown length
2334: contig of 1295 bp in length
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AC012536.2 GI:6479135
HTG: HTGS_PHASE1: HTGS_DRAFT.
        Db 82915 CCACCGCACCTGGCTGATG 82933
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TITLE JOURNAL

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repeat_region /uvc="match repeat: matches 400. .430 or consensus"

//uvc="match repeat: matches 262. .117 of consensus"
//uvc="match repeat: matches 85. .301 of consensus;
//uvc="match repeat: matches 85. .301 of consensus;
//uvc="match repeat: matches 1. .337 of consensus;
//uvc="match repeat: matches 1. .337 of consensus"
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complement(join(26546. .26932,27171. .27347,27446. .27524,
7782. .27861,29276. .29347,29456. .29570,29695. .29742,
30178. .30207,30365. .30473,33547. .33605,34826. .34955,
35525. .35905)
                                                                                                             incomplete repet" matches 364. .1 of consensus" 13595. .13953. .13953. .13953. .13953. .139546. .13972. .14648 /note="LiMC3 repeat: matches 1676. .2345 of consensus" 14649. .15978 /note="LiMC3 repeat: matches 1. .301 of consensus" 14949. .15077 /note="LiMC3 repeat: matches 2336. .2470 of consensus" 15102. .15231 /note="FiAMA repeat: matches 133. .4 of consensus" 15244 .15289
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complement(join(26853. .26932,27171. .27347,27446. .27524,
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24456. .24530

24456. .24530

Anote="match: ESTS R50012 R70180"

24555. .2481 repeat: matches 41. .123 of consensus"

24535. .2483 repeat: matches 302. .1 of consensus"

24840. .2518

Anote="LIMC2 repeat: matches 1065. .772 of consensus"

25136. .25452

Anote="MALD repeat: matches 11. .302 of consensus"

25649. .25765

Anote="MERSA repeat: matches 63. .189 of consensus"

25130. .25545

Anote="MERSA repeat: matches 63. .189 of consensus"

26130. .25545

Anote="MITLB repeat: matches 1. .390 of consensus"

Complement(22546. .35701)
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/product="dJ179N16.1 (Stress Activated Protein Kinase
(Mitogen Activated Protein Kinase p38delta))"
complement(26546. .35905)
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16823. .16969

7hote="MER11A repeat: matches 4. .151 of consensus"

16868. .17594

7hote="MER11A repeat: matches 60. .738 of consensus"

17278. .17886
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"23 copies of 2 mer 100 % conserved" 15574. 15853
7/note-"match: Z63849 CpG Island clone 91cli
16341. 16702
           .217 of
                                                                                           . 288
                                                                                         205.
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              matches
                                                                                           matches
        /note="AluSq repeat: mincomplete repeat"
13494. 13581
/note="AluSx repeat: m
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                                                                                                                                               Park
sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The true left end of clone 179N16 is at 1 in this sequence. The true right end of clone 548E15 is at 690.
The true left end of clone 179N16 is at 172048.
179N16 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5986. .6284
/note="AluJb repeat: matches 1. .296 of consensus"
6361. .6420
/note="AluSx repeat: matches 301. .242 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .574 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7809. .8170
/note="1.1MC2 repeat: matches 15. .384 of consensus"
8255. 83.78
/note="MER2 repeat: matches 13. .136 of consensus"
8396. .8603
/note="AluJb repeat: matches 291. .82 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1 repeat: matches 5082. .4624 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .465 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .209 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5387 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .62 of consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 106. .248 of consensus" 12735. .13031
//note="Alusx repeat: matches 1. .298 of consensus" 13042. .13256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1208. .4497
/note="AluJb repeat: matches 289. .1 of consensus"
5473. .5894
/note="MLTIC repeat: matches 39. .465 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 300. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .463 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .874 of
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note="13 copies of 2 mer 96 % conserved"

10970. .11269

note="AluSg repeat: matches 300. .1 of co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .133 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1714. .1954
/note="LIMB8 repeat: matches 324.
1956. .2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 734 mote="AluJo repeat: matches 302. ncomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1605. 8691

Anote="MER2 repeat: matches 125.

8826. 8890

Anote="MER2 repeat: matches 279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621. .7941
note="L1 repeat: matches 5068.
809. .8170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1518. .9894
note="THE1C repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .612. .6914
'note="AluJb repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1...1077)
/note="match: STS AL020972"
4..457
                                                                                                                                                                                                                                                       1. .172048
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3168. .3369
/note="MER44C repeat:
1208. .4497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6951. .7084
/note="FLAM_C repeat:
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note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                     /clone="RPI-179N16"
/clone_lib="RPCI-1"
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6612. .6914
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3605. .8691
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Query Match
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HUMVIPHM1
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                                                                                                                                                                                                                                                 /translation="MSLIRKKGFYKODVNKTAWELPKTYVSPTHYGSGAYGSVCSAID
KRSGEKVATKKLSRPPQSETFAKRAYRELLLIKHWGENVIGILLDVFTPSSELRNFYD
FYLVMPFMQTDLQKIMGMEFSEEKTOYLVYQMLKGLKYTHSAGVVHRDLKPGNLAVNE
DCELKILDFGLARHADAEMTGYVYTRWYRAPEVILSWMHYNOTVDIWSVGCIMAEMLI
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Homo sapiens clone hRPK.90_A_1, *** SEQUENCING IN PROGRESS ***, 2
ordered pleces.
.29742,
                                                                                                                                               4
                                                                                                                       /evidence=not_experimental
/product="dJ179N16.1 (Stress Activated Protein Kinase
(Mitogen Activated Protein Kinase p38delta))"
/protein_id="CAB08438.1"
/db_xref="G1:3036774"
/db_xref="SPTREMBL:015264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 204027)
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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This sequence will be replaced by the finished sequence as soon as it is available and
.29347,29456. .29570,29695. .30473,33547. .33605,34826.
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                                                                                                                                                                                                                                                                                                                                                     Length 172048;
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                                                                              /note="match: proteins 014739 015124"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                     DB 10;
1.5;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Pred. No.
.27861,29276. . .30207,30365. . .35643)
                                                                                                                                                                                                                                                                                                                                        13.9%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 41760 CCACCGCACCTGGCTGATG 41742
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HTG; HTGS_PHASE2.
27782. .27861
30178. .30207
35525. .35643
/gene="SAPK4"
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCACCGCACCTGGCTGATG 19
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Best Local Similarity 100.
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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JOURNAL
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TITLE
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REFERENCE
AUTHORS
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AC007158
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human vasoactive intestinal peptide and histidine-methlonine amide peptide hormone (VIP/PHM-27) gene, exon 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M14618.1 GI:340266
histidine-methionine amide; hormone; peptide hormone; vasoactive
intestinal peptide.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Linders 1 to 270)

Linders, Barkhem, T., Norberg, A., Persson, H., Schalling, M., Hokfelt, T. and Magnusson, G.

Structure and expression of the gene encoding the vasoactive intestinal peptide precursor

Proc. Natl. Acad. Sci. U.S.A. 84 (2), 605-609 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA (libraries of Lawn and EMBL), clones lambda-VIP-D lambda-VIP-4.
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the accession number will be preserved 1 160375; contig of 160375 bp in length 160376 204027; contig of 43652 bp in length.
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                                                                       Location/Qualifiers
1. 204027
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hRPK.90_A1"
/clone="hRPK.90_A1"
/clone="hRPK.90_A1"
/clone="hRPK.90_A1"
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                                                                                                                                                                                                                                                                     Score 19; DB 42;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="VIP/PHM27 mRNA intron 67 c 69 g 58 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 6.7
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                     13.9%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                    DD 111376 CCACCGCACCTGGCTGATG 111394
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                                                                                                                                                                                                                                                                       Query Match 13.9
Best Local Similarity 100.
Matches 19; Conservative
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G24450
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/product="SWI/SNF" complex 155 KDa subunit"
/product="SWI/SNF" complex 155 KDa subunit"
/product="SWI/SNF" complex 157 KDa subunit"
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NEWMNEEDDYEVDERREYSFROREEDGOBDLTKDAGGRAAARRKHYREYTU-TOTTIL
NESTRANGGTAAAARAALEFFNGRKKSCREDEDPARGDOSREYDGEDNATTOTTILI
IPSTAABFDYNCIHVIERRALPEFNGRKKSCREDEDPARGDOSREYDGEDNATTOTTILI
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ASDLRSPQVPAAQONLAFPERNEKEVDLONFGLRTDIYSKRTLAGFSGRATE
QETLLLLEALLENTKSDWNKVSTYRELGAARGSCREATEGAEFSRRKESDYLENDSGAGRAT
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Purification and biochemical heterogeneity of the mammalian SWI-SNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETDEGDKAQDGENEKNSEKEQDSEVSEDTKSEEKETEENKELSSTCKERESDTGKKKV
ETBELSEGNYATAAAALASAATKAHLAAVEERK IKSLVALLVETQMKKLEIKLRHFE
GLETIMDREKALEQQRQQLITERQNHEMDGLKYAELRARQMEQQDHGQNPQQAHQH
SGGPGLAAPLGAAGHGGMPPPYPLMHHQMPPHPDPOGOIPGFGSMMPGQHMPG
RMIPTVAANIHPSGSGPTPPGMPPMGNILGPRVPLTAPNGMYPPPPQDPD
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                                                                                                                                                                                                                                                                   Wang, W., Xue, Y., Zhou, S., Kuo, A., Cairns, B.R. and Crabtree, G.R. Diversity and specialization of mammalian SWI/SNF complexes Genes Dev. 10 (17), 2117-2130 (1996)
                                                                                                                                      Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5190)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                         GI:1549238
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Matches
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TITLE
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AUTHORS
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LOCUS HSUG6615 5190 bp mRNA PRI 18-SEP-1996
DEFINITION Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                  Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                        Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
      31-MAY-1996
                                                                                             G24450.1 GI:1344776
STS; STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research S cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Location/Qualifiers
1. .474
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   G24450 474 bp DNA site. Shuman STS WI-13939, sequence tagged site.
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117 c 101 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer A: CCTCCCTTTTCATTACCAC
Primer B: GTCAGAGAGTCTTCCCGAGG
STS size: 150
PCR Profile:
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Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taq Polymerase: 0.025
Total Vol: 20 ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Hudson
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Primer: each 5 pM
dNTPS: each 4 nM
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Tris-HCL: 10 mM
pH: 9.3
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                                                                                                                                                                                                                                   Homo sapiens
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Gaps

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Submitted (14-MAX-1997) Whitehead Institute/MIT Center for Genome Submitted (14-MAX-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases I to 23536)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, T., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Garajgery, K., Gilmartin, T., Grant, G., Hages, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Maddrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, K., Roberts, D., Rossello, R., Styne, C., Strickland, C., Subramanian, A., Torruella Miller, I., Vassillev, H., Vola, Wagner, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chases 1 to 23536)
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W.,
Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P.,
Barna, N., Chang, A., Cooke, P., Daly, M.J., Forrest, C., Fripp, W.J.,
Gage, D., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzle, J.,
Marquis, N., McDermott, J., Molloney, N., Morrow, J., Machman, A.,
Naylor, J., O'Connor, T., Peterson, K., Rollins, G., Spencer, J.,
Stilwell, J., Stone, C., Strickland, C., Sydney, K., Wilmer, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Only 23.5 kilobases of this clone are being submitted. The remainder overlaps either accession number AC000393 (WICGR project L174) or accession number AC000394 (WICGR project L177).
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Location/Qualifiers
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Submitted (31-JUL-1998) Whitehead Institute/MIT Center for Genome Submitted (31-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 31, 1998 this sequence version replaced gi:3184311.
All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)
                                                                                                                                                                                                          Gaps
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Homo sapiens chromosome 9q34, clone 182E8, complete sequence.
AC002120
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhin: Hominidae: Homo.
1 (bases 1 to 21536)
Birren,B., Fasman,K., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 9934, clone 182E8
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                                                                                                                                             Length 14837;
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6.1;
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/clone="CITB-H1_2129G21"
3077 c 3067 g 4254
                                                                                                                                                13.1%; Score 18; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                 HTG 03-AUG-1999
Homo sapiens chromosome 5 clone CITB-H1_2129G21, *** SEQUENCING IN ACKORESS ***, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished

2 (bases 1 to 14837)

2 Date Second Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1487)
DOE Joint Genome Institute.
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www.jgl.doc.gov.
www.jgl.doc.gov.
*ww.jgl.doc.gov.
*ww.jgl.doc.gov.
*working draft' sequence. It currently
*consists of 18 contigs. The true order of the pieces
*s is not known and their order in this sequence record is
*arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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contig of 644 bp in length
gap of unknown length
contig of 1387 bp in length
gap of unknown length
contig of 1390 bp in length
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g of 649 bp in length
f unknown length
g of 122 bp in length
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g of 1018 bp in length
f unknown length
g of 898 bp in length
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gap of unknown length
contig of 1022 bp in length
gap of unknown length
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/db_xref="taxon:9606"
/chromosome="5"
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AC008821/c
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REFERENCE
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repeat_region

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1. .23536
/organism="Homo sapiens"
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/clone="1828"
/clone="1828"
/clone="1828"
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/chromosome="
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/rpt_family="LIMC2"
complement(14203, 14225)
/rpt_family="(TA)n"
14992, 15140
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complement(12478. .12512)
/rpt_family="MIR"
complement(12789. .12913)
/rpt_family="(GGA)n"
13842. .14006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5200...5496)
/rpt_family="Alusx"
complement(5828..5928)
/rpt_family="L2"
5978..6111
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complement(6824. .7114)
/rpt_family="AluJb"
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/rpt_family="L2"
10625..11063
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6112. .6413
/rpt_family="Alusp"
complement(6782. .6812)
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/rpt_family="AluJo"
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cpt_family="(TGGA)n"
1878. .11996
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1998. ,12100
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3493. .3520
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15187. .15494
/rpt_family="AluJb"
15509. .15936
/rpt_family="LlM4"
15939. .16234
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/rpt_family="L1M4"
16796. .17086
/rpt_family="Alusg"
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1366. 1150.
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4310, 4406
/rpt_family="(GA)n"
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1681. 1100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Uncertain number of A's; either 24, 25, complement(22159. .22762)
/note="Single-stranded terminator coverage."
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/note="Single-stranded terminator coverage."
complement(21284. .21555)
/rpt_famlly="Alusg"
21579. .22388
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complement(19559. .19580)
/note="Single-stranded coverage."
19632. .19779
                                                              18073. .18370
/rpt_family="Alusx"
complement(18154. .18174)
/note="Single-stranded coverage."
18372. .18838
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/rpt_fanily="TigGER1"
complement(23460. .23493)
/rpt_family="LiMB3"
complement(23500. .23535)
/rpt_family="Alu"
a 5475 c 6200 g 5404 t
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18643. .19029
/rpt_family="LIME3A"
complement(19050. .19522)
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21582
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2996. .23288
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.9888. .20108
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17277. .17581
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17723. .18068
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18073. .18370
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19781, 1007
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/rpt_family="MLTlA2"
20109. .2043=
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20436. .20726
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23291. .23760
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20805. .21205
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22686. .22994
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NNA HTG 16-NOV-1999
*** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
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/rpt_family="Alu"
complement(18386. .18965)
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/rpt_family="Alu"
complement(32818, 32919)
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complement(29341. .29831)
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/fpt_family="MIR"
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/rpt_family="Alu"
9325. .9613
/rpt_family="Alu"
10632. .10680
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28658. .28950
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8121 c 8156 c
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complement(12178.
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complement(22974.
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complement(13207.
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complement(25246.
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30332. .30627
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11827. .1200
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"Template

"Deases 1 to 33602)

Resears (G.A., Bardbury, Brignac, S., Bumeister, R., Davie, J.,

Davies, G.A., Bardbury, Brignac, S., Bumeister, R., Davie, J.,

Davies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L.,

Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hanher, L., Harris, J.,

Hinson, S., McFarland, J., Megarity, C., Narayanaswamy, U., Newton, J.,

O'Brien, K., Oliver, T., Patel, P., Probst, S., Rayner, S.,

Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D.,

Nard, T. and Wilson, R.

Direct Submission

AL Submitted (O'O-OT-1996) McDermott Center for Human Growth and

Development, University of Texas Southwestern Medical Center at

Dalsas, 5323 Harry Hines Blvd, Dallas, Ty 75235-8591, USA

3 (bases 1 to 33602)

Evans, G.A., Bradbury, P., Brignac, S., Bumeister, R., Burbee, D.,

Ranklin, T.L., Garner, H.R., Gordon, M., Gotway, G., Grant, O.,

Hahner, L., Harris, J., Hinson, S., Megarity, C., Narayanaswamy, U.,

Newton, J., O'Brien, K., Ollver, T., Patel, P., Probst, S., Rayner, S.,

Rand Wilson, R., Schultz, R., Syed, M., Valenzuela, D.,

Blirett Submission

Direct Submission
                                                                                            Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Joses 1 to 33602)

Bovas, G.A., Bradbury, P., Brignac, S., Bumeister, R., Burbee, D., Bovie, J., Davies, C.J., Davies, C.J., Pondon, T., Eranklin, T.L., Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hanson, S., Megarity, C., Narayanawamy, U., Hancon, J., Garner, M., Gordon, M., Gotway, G., Grant, O., Gordon, M., Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-UUL-1997) Genome Science and Technology Center, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA On Jul 24, 1997 this sequence version replaced gi:1737198.

Location/Qualifiers
1. 33602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cSR134e5"
/chromosome="ll"
complement(448. 727)
/rpt_family="Alu"
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/rpt_family="Alu"
complement(2890. .3084)
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complement(3654. .3938)
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/rpt_family="Alu"
complement(7621. .7793)
/rpt_family="MIR"
8519. .8779
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820. .6110
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complement(2027. .2078)
/rpt_family="Alu"
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6852. .7070
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336. .6591
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U73643
U73643.1 GI:2276400
                                                                                Homo sapiens
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.166 of consensus"

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Justic . 10000

/ note="Alusa repeat: matches 11. .301 of consensus"
10895. 11535
/ note="Libra repeat: matches 271. .910 of consensus"
11579. 11683
/ note="Libra repeat: matches 6. .109 of consensus"
11696. 11997
/ note="Alusa repeat: matches 4. .302 of consensus"
12035. 12536
/ note="Aluxa repeat: matches 166. .685 of consensus"
complement(12862. .>13184)
/ note="match:STS L40936"
13500. 13500
/ note="match:STS repeat: matches 2. .302 of consensus"
13554. 13646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7555. 7686

7665. 7686

7601-11 repeat: matches 5150. 5270 of consensus.

7689. 7991

7001-11 repeat: matches 1. .300 of consensus.

7995. 9210

7001-11 A328

70011. 8328
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8960. .9262
/note="AluJo repeat: matches 1. .302 of consensus"
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/note="L1 repeat: matches 3627. .3966 of consensus"
5093. .5238
/partial
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/note="L1 repeat: matches 3985. .4239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6224. .6574
/note="11 repeat: matches 4377. .4731 of consensus"
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/note="Aluub repeat: matches 300. .1 of consensus" 4296 .4599
/note="Aluub repeat: matches 2. .302 of consensus" 4765. .5092
                                                                                                                                                                                                                                                                                /note="Alusg repeat: matches 1. .146 of consensus" 239. .5543 /note="Alux repeat: matches 1. .301 of consensus" 5545. .5710 /partial
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//note="Alusx repeat: matches 302. .3 of consensus"
10310. .10600
                                                                                2362. .2662
Moote-"Aludb repeat: matches 1. .302 of consensus"
3815. .4132
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Mote="LiMA10 repeat: matches 297.
                                             1986. .2286
/note="%1usx repeat: matches 1.
2362. .2662
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1338. .8411
Partial
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hote="AluJo repeat: matches 2.
8747. .8957
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          matches
        /note="FRAM repeat: match
complement(960. .1259)
/note="match:STS G05254"
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8451. R741
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Rockville, MD, USA
This sequence was identified as CDM:10212742 by the submitter.
This sequence was identified as CDM:10212742 by the submitter.
* For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* Location/Qualifiers
1. 35967
/ Organism="Drosophila melanogaster"
/ db_xref="taxon:7227"
10857 a 7230 c 7235 g 10645 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deadman, R.

Direct Submission
Submitsed (13-NOV-1996) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RO, UK E-mail enquires: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is not the entire insert of clone 506G2.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA PRI 23-NOV-1999
PAC 506G2 contains STSs and a CpG island.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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296. .596
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/note="AluSp repeat: matches 1. .302 of consensus"
604. .772
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163. .281
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/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                 13.1%; Score 18;
100.0%; Pred. No.
tive 0; Mismatch
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/clone_lib="RPCI-3"
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/partial
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Matches 18; Conserv
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34644. .34800
/note="MLT2_internal repeat: matches 2419. .2264 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusg repeat: matches 1. .296 of consensus" 30955. .31101  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                              .300 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote-"11 repeat: matches 3151, .3280 of consensus" 29553, .29796
/note-"MLT2_internal repeat: matches 5375, .5124 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MLT2_internal repeat: matches 4572. 3316 of
                                                                                                                                                            15714. 16016

//note="AluJb repeat: matches 1. .290 of consensus"
//note="FLAM_A repeat: matches 117. .6 of consensus"
//note="FLAM_A repeat: matches 117. .6 of consensus"
//note="FLAM_A repeat: matches 117. .6 of consensus"
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/note="AluY repeat: matches 3. .300 of consensus" 26761. .27058
/note="AluSp repeat: matches 2. .302 of consensus" 27676. .27988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ō
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                                                             matches 13. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Alusx repeat: matches 1. .298 of consensus" 28413. .28685
/note="Alusx repeat: matches 298. .2 of consensus" 28718. .28848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30324. .30621
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30655. .30952
                                                                                                                                                                                                                                              "note="Alusp repeat: matches 303. .2 of consensus"
9497. .19756
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/note="MLT2_internal repeat: matches 4754. .4572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .890 of
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23783. .23828
/note="23 copies of 2 mer 80 % conserve
24117. .24481
/note="LIPAS repeat: matches 517. .890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus"
33199. .33502
/note="AluJo repeat: matches 1. .302
33616. .33917
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14722. 15024
/note="AluSx repeat: matches 1.
15222. 15326
/partial
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Chases to 44294)

Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W.,
Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P.,
Barna,N., Brown,K., Cooke,P., Dally,M.J., Forrest,C., Fripp,W.J.,
Gage,D., Geraigery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzle,J.,
Marquis,N., McDermott,J., Molloney,N., Morrow,J., Nachman,A.,
Maylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J.,
Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-APR-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
(bases 1 to 44224)
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W., Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P., Barna, M., Chang, A., Cooke, P., Daly, M.J., Forrest, C., Fripp, W.J., Gage, D., Geraigery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J., Marquis, N., McDermortt, J., Moloney, N., Morrow, J., Wachman, A., Maylor, J., O'Connor, T., Peterseon, K., Sthins, G., Spencer, J., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Wilmer, F. and
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Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 29, 1997 this sequence version replaced g1:1929461. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                       Gaps
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1e; Homo.
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                                                                                                                                                                 of
                                     .301 of consensus'
                                                                                                                                                                 .1754
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1 (bases 1 to 44294)
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W., Fasman, K.H. and Lander, E.S.
Genomic sequence from Human 9934
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                                                                                                                                                                                                                                                              Length 37027;
                                                                                            35350, .35569 // Arternal repeat: matches 1972. consensus"
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6;
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Conservative 0; Mismatches
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Query Match 13.1%; Score 18; DB 10; Length 44294; Best Local Similarity 100.0%; Pred. No. 5.9; Matches 18; Conservative 0; Mismatches 0; Indels 0. repeat_region /rpt_family="AluJb"
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                                                                                                                                                                                                                                             Direct Submission

Submitted (23-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Oct 31, 1999 this sequence version replaced gi:6102621.

*WWW.jgi.doe.gov.

*WOTE: This is a 'working draft' sequence. It currently

*Consists of 23 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* Inns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                     HTG 31-OCT-1999 PROGRESS ***, 23 unordered pieces.

HTG 31-OCT-1999
ACG SA**, 23 unordered pieces.
                                                                                                                          Homo sapiens
Eukaryota: Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 451 bp in length gap of unknown length contig of 715 bp in length contig of 842 bp in length gap of unknown length gap of unknown length
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contig of 842 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                            700: contig of 700 bp in length
gap of unknown length
3126: contig of 2426 bp in length
gap of unknown length
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of 2137 bp in length
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of 765 bp in length
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Sequencing of Human Chromosome 19
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DOE Joint Genome Institute.
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HTG: HTGS_PHASE1.
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AUTHORS
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KEYWORDS
SOURCE
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JOURNAL
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COMMENT

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Exercises 1 to 55707)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckelly, R., Boguslavkiy, L., Boukhgalter, B., Barown, A., Castlera, C., Collymore, A., Cochangelo, M., Collins, S., Collymore, A., Cocke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhlano, K., Dewar, K., Domino, M., Morada, J., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Lock, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Marjor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Stanger Thomann, N., Stofanon, T., O'Donnell, P., Stanger Thomann, N., Stofanon, T., O'Donnell, P., Stanger Thomann, N., Stofanon, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Liss Submission

Al repeats were identified using Repeathmasker: Smit, A.F.A. 6

Green, P. (1996-1997)

** NOTE: This record contains 63 individual

** sequencing reads that have not been assembled into

** contigs. Runs of N are used to separate the reads

** and the order in which they appear is completely

** arbitrary. Low-pass sequence sampling is useful for

** contigs. Runs of N are used to separate the reads

** and the order in which they appear is completely

** arbitrary. Low-pass sequence sampling is useful for

** the record is updated, the accession number will

** becaused to completion. In the event that

** the record to completion. In the event that

** beginning to the sequenced to completion. In the the that

** the record to completion. In the that

** the record of the order that

** the record of the order of the accession number will
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Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                           17 others
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40884: contig of 6016 bp in length
gap of unknown length
48925: contig of 8041 bp in length.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 55707)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone 115_K_14
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1. 48925
/organism='Homo sapiens"
/db_xref='raxon:9606"
/chromosome="LLNL-F_143B12"
a 12710 c 12124 g 11601 t
34868: contig of 3911 gap of unknown
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100.0%; Pr
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HTG: HTGS_PHASE0.
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RESULT 30
AB026647
LOCUS AB026647 81542 bp DNA PLN 07-MAY-1999
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MJL12,
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Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
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/clone="115_K_14"
/clone="11b="RPCI-11 Human Male BAC"
a 10660 c 10769 g 17182 t 699 others
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2391. .2691
/note="AluSx
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8616. .8
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8743. .8
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La Submitter R.

Direct Submission

La Submitter (24-28P-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Sep 18, 1998 this sequence version replaced gi:3550203.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
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                                                                                                                                          Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
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Human DNA sequence from clone 931E15 on chromosome Xq25. Contains
STSs, GSSs and genomic marker DXS8098, complete sequence.
AL023575
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                                                                                Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                               Submitted (28-APR-1999) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail;ynakamu@Kazusa.or.jp, Tel:81-438-52-3935(ex.7443),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 81874)
                                                                                                                                                                                                                                                           Structural Analysis of Arabidopsis thaliana Chromosome 3.
Unpublished (1999)
2 (bases 1 to 81542)
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14006 c 14834 g 26843
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/db_xref="taxon:3702"
/chromosome="3"
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100.0%;
complete sequence.
AB026647
AB026647.1 GI:4757403
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HTG; DXS8098.
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These 18; Conservative
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HS931E15/C
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This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X human chromosome X, constructed by the Sanger Centre Chromosome X happing Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX 931E15 is from the library RPC15 constructed at the Roswell Park Garcer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 IMPORTANY: This sequence is not the entire insert of clone 931E15. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of 424/12 (282207) is at 3643 in this sequence. The true right end of 50662 (282213) is at 37431.
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sequence is ambiguous, there is an annotation using the 'unsure'
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// note="L1 repeat: matches 3627. .3966 of consensus" 5498 .5643
// note="AluX repeat: matches 1. .146 of consensus" 5644. .5948
// note="AluX repeat: matches 1. .301 of consensus" 5950 .6115
// note="AluX repeat: matches 133. .290 of consensus" 6156. .6393
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/note="AluY repeat: matches 228. .301 of consensus"
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/note="il repeat: matches 4377. .4731 of consensus" 6798. .7073
/note="mark? repeat: matches 1. .95 of consensus" complement(7078. .7139)
/note="mark? repeat: matches 345. .284 of consensus"
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8094. .8396
/note="Alux repeat: matches 1. .300 of consensus"
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/note="AluSp repeat: matches 1. .302 of consensus"
1010. .1178
1010. matches 5. .166 of consensus"
complement(1365. .1664)
/note="match: STS G05254"
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/2067. .3067
/2068-"AluJb repeat: matches 1. .302 of consensus"
complement(4220. .4537)
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/note="AluSx repeat: matches 1. .293 of consensus"
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/note="AluJb repeat: matches 300.
4701. .5004
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/db_xref="taxon:9606"
/chromosome="X"
/map="q25"
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/clone_lib="RPCI-5"
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/note="L1 rep
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AC004472 86765 bp
Homo sapiens chromosome
AC004472
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2 (bases 1 to 86765)
Lamerdin, J.E.
                                                                                                consensus
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AUTHORS
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                                                                                                                                            //oce="AluSx repeat: matches 7. 301 of consensus"
11299. .11939
//oce="LipA8 repeat: matches 271. .910 of consensus"
11981. .12087
//oce="LipA8 repeat: matches 6. .109 of consensus"
12100. .12401
//oce="AluSx repeat: matches 4. .302 of consensus"
12439. .12940
//oce="AluSx repeat: matches 166. .685 of consensus"
12439. .12940
//oce="matche: TS L40336"
//oce="matche: TS L40336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n complement(17160. 17224)
/note="MIR repeat: matches 149. .84 of consensus"
18120. .18226
/note="match: STS L24586"
complement(18124. .18827)
/note="match: GSS B16853 B14990"
complement(18378. .19676)
/note="match: 20160
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Aluyb repeat: matches 196. .300 of consensus"
fiel18. 16420
/note="Aluyb repeat: matches 1. .290 of consensus"
complement(16828. .16935)
                                                                                                                                                                                                                                                                                                                /note="AluJo repeat: matches 2. .300 of consensus" 9152. .9362
/note="AluJo repeat: matches 87. .299 of consensus" 9365. .9667
/note="AluJo repeat: matches 1. .302 of consensus" 9668. .10289
/note="LiMA10 repeat: matches 297. .919 of consensus"
                                                                                                complement(10371. 10670)

Anote="Alusx repeat: matches 302. .3 of consensus" (10710. 11004
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.5626. .15730
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.

La (bases I to 8675)

La (bases I to 8676)

Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Garnes, J., Danganan, L., Poundatone, P., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.O.
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Submitted (25-MAR-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
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9, Pl clone 11659, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                     30728. 31025
/note="AluSx repeat: matches 1. .299 of consensus"
31059. 31359. 31505
/note="MLSX repeat: matches 1. .296 of consensus"
31359. 31505
/note="MER4B repeat: matches 11. .148 of consensus"
32041. 32319
/note="MLSX repeat: matches 11. .287 of consensus"
complement(32381. 33599)
/note="AluSx repeat: matches 1. .298 of consensus" complement(28817. .29089)
//note="AluSx repeat: matches 298. .2 of consensus" 2012. .29252 //note="Il repeat: matches 3151. .3280 of consensus" complement(29957. .30200)
//note="MLT2_internal repeat: matches 5375. .5124 of
                                                                                                                                                                                                                                                                                                                 /note="MLT2_internal repeat: matches 4754. .4572 of
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33603. .33906
Anote-"Aludo repeat: matches 1. .302 of consensus"
34020. .34321
/note-"Aludb repeat: matches 1. .301 of consensus"
complement(34388. .34933)
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/organism="Homo sapiens"
/dLxref="taxon:9606"
/clone="Pi.11659"
/chzomosome="9"
                                                                                                                                                                                                                                                                          complement(30513. .30706)
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/rpt_camily="Alusq"
/rpt_camily="Alusq"
1714. .18004)
/rote="DDS similarity to overlapping ESTs:-(17788. .18004)
AA05473 zf51a08.r1 Soares retlina N2b4HR Homo saplens cDNA
clone 380438 5' similar to contains Alu repetitive
element; (276. .1); 99% identity.-(18004. .17714) A013121
ze26007.r1 Soares retlina N2b4HR Homo saplens CDNA clone
360108 5' similar to contains Alu repetitive element;
(1. .292); 97% identity.-(18004. .17714) AA01750.
ze38h03.r1 Soares retlina N2b4HR Homo saplens cDNA clone
361301 5' similar to contains Alu repetitive element;
Score: 567 identity: 292/297 (98%)."
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/rpt_family="AluJb"

n complement(21817...21953)

/rpt_family="MiR"
22765...2291

/rpt_family="MiR"
22765...2291

/rpt_family="MiR"
22810...22867

/rpt_family="GAAD,n"
22810...22867

/rpt_family="GAAD,n"
24453...24713

/note="DDS similarity to A382319 EST95595 Testis I Homo sapiens CDNA 5' end. Score: 505 Identity: 258/260 (99%)."
25318...2587

/note="DDS similarity to AA061824 ml33d04.rl Stratagene mouse testis (#937308) Mus musculus CDNA clone 513799 5', 51318...2587 Identity: 295/437 (67%).--(25480...25887)

Score: 279 Identity: 295/437 (67%).--(25480...25887)

BLASTN similarity to AA860210 (1...407); match: 1, score: 5.7e-157; database searched: month.na; ak48c12.sl Soares testis INTH Homo sapiens CDNA clone IMAGE:1409206 3'"

/rpt_family="MLTID"
AA013249 ze26c07.s1 Soares retina N2b4HR Homo sapiens CDNA clone 360108 3' similar to gb.M3563 INTERFERON-INDUCED, DOUBLE-STRANDED RNACTIVATED FROTEIN KINASE (HUMAN); contains Alu repetitive element; Score: 645 Identity: 359/370 (97%).--(15334. .1556) AA016313 2c38h03.s1 Soares retina N2b4HR Homo sapiens CDNA clone 3613013 ' similar to gb.M3563 INTERFERON-INDUCED, DOUBLE-STRANDED RNA ACTIVATED PROTEIN KINASE (HUMAN); contains Alu repetitive element; Score: 449
                                                                                                                                                                                                                                                                                                                                                /note="DDS similarity to AA054173 zf51a08.rl Soares retina N2D4HR Homo sapiens cDNA clone 380438 5' similar to contains Alu repetitive element; (416. .277); 99%
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complement(2124. .21361)
/rpt_family="MIR"
21365. .2140-
                                                                                                                                                                                                      complement(18516. .18710)
/rpt_family="AluJo"
18906. .19203
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/rpt_fam1ly="Alux"
19288. .20021
/rpt_fam1ly="LINE2"
20258. .20313
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|7188. 1
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15334. .15566
/note="DDS similarity to overlapping ESTs:-(15334. .15694)
                                       /note="Pl clone obtained from Genome Systems, Inc." complement(4. .80) /rpt_family="MER4_internal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MER4_internal"
complement(7560. .8234)
/rpt_family="MER4A"
8239. .914
                                                                                                                                       complement(402..626)
/rpt_family="MER4_internal"
complement(707..1338)
/rpt_family="HERVH"
complement(1361..1741)
/rpt_family="HERVH"
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/rpt_family="AluJo" complement(10495. 10794)
/rpt_family="AluSg" 11777. 17072
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rpt_family="MER4_internal"
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/rpt_family="MSTB-internal"
complement(9215. .9483)
/rpt_family="AluJo"
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841. .10206
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crpt_family="Alux"
crpt_family="LINE2"
13809. .13944
                                                                                                                                                                                                                                                            complement(1742. 3015)
/rpt_family="HERVH"
complement(3388. 4084)
/rpt_family="HERVH"
complement(4145. 4571)
/rpt_family="HERVH"
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complement(5036. 5671'
/rpt_family
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/rpt_family="MER83"
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2479. .1277
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/rpt_family="Alus"
5734. .6025
/rpt_family="Alusx"
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4620 11000
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5118. .15404
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2077
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.3945. 14047
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[4896. .15064
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complement(10291.
                                                                                                                       /rpt_family="AluY"
complement(402. .6:
                      /lab_host="NS3516"
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join(-9687. .9877,12970. .13052,20256. .20352,22663. .22821,38387. .38467,49399. .49564,58705. .58813,60343. .>60512)
/gene="day398222.1"
/note="f46-like contains exons 2-9 continues in 284478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="Card Fig.)
//db_xref="G1:2956661"
//db_xref="G1:2956661"
//db_xref="G1:2956661"
//db_xref="SPTREMBL:014998"
//db_xref="SPTREMBL:0149988"
//db_xref="SPTREMBL:014998"
//db_xref="SPTREMBL:014998"
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//db_xref="SPTREMBL:
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NTELLGYLQVFPGLLERVIDLLRVIHVAGKETTNIFSNCGCVRAEGDISNVANGFKSH
LIRLIGNLCYKNKDNQDK"
                                                                                                                                                                                                                             /map="22q11.2-qter"
/clone="RP3-398022"
/clone=lib="RPC1-3"
511. .575
/note="AluJb repeat: matches 296. .232 of consensus;
incomplete repeat: matches 153. .3 of consensus;
incomplete repeat: matches 153. .3 of consensus;
incomplete repeat: matches 300. .2 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="dj398C22.1 (novel protein, ortholog of mouse brain protein E46)"
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700te-"Aluub repeat: matches 1. .302 of consensus"

11343. .11559

700te-"Min repeat: matches 223. .30 of consensus"

11588. .11877

700te-"Alusy repeat: matches 1. .291 of consensus"

11942. .12099

700te-"MIR repeat: matches 86. .259 of consensus"

11367. .13632

700te-"Min repeat: matches 358. .1 of consensus"

13635. .13927
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14474. .14770

/note="AluSp repeat: matches 1. .297 of consensus"

14771. .14934

/note="AluSx repeat: matches 138. .302 of consensus; incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /noce="Mill repeat: matches 44. .358 of consensus" 13947. .14046 / hote="MIR2 repeat: matches 109. .15 of consensus" 14344. .14473 / hote="AluJb repeat: matches 1. .131 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4898 of consensus"
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/note="AluJo repeat: matches 302. .1 of consensus"
6512. .6809
/note="AluSg repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7753. .8041
/note="AluSg repeat: matches 1. .290 of consensus"
9331. .9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wir repeat: matches 38. .251 of consensus"
9687. .60512
/gene="dJ398C22.1"
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Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       011. .3311
note="AluSx repeat: matches 1. .301 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 5042.
                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                           /chromosome="22"
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/note="L1 re
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                                                                   FEATURES
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L Submitted (31-JUL-1997) Chromosome 22 Project Group
(http://www.sanger.ac.uk/HGP/Chr22/) Sanger Centre, Hinxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Aug 7, 1997 this sequence version replaced gi:1929050.
IMPORTANT: This sequence is not the entire insert of clone 398C22.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre chromosome 22
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true right end of clone 941F9 is at 104.
The true right end of clone 398C22 is at 89328.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(29214. .29339)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 50.000"
complement(29628. .29915)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens DNA sequence from PAC 398C22 on chromosome 22G11.2-qter. Contains Brain Protein E46 like sequences, 293784
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0
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100.0%; Pred. No.
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22q11.2-qter; Brain Protein E46-like.
                     /rpt_family="AluJb"

complement(26831.27035)

/rpt_family="MLTID"

complement(27042.27333)

/rpt_family="Alux"

complement(27342.27637)

/rpt_family="AluSp"

complement(27344.27637)
                                                                                                                                                                                                                                                      /rpt_family="MLT1D"
27727. . . 2801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'rpt_family="7SLRNA"
                                                                                                                                                                                                                                                                                                                                                                                      Z8681. .28972
/rpt_family="Alusx"
29177. ??**
                                                                                                                                                                                                                                                                                                                                 7727 .28020
rpt_family="Alusx"
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Best Local Similarity
Matches 18; Conserv
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HS398C22
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
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COMMENT

SOURCE

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Gaps

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Length 89328; Indels

DB 11; 5.8;

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Lamerdin, J.E., Kyle, A., Elliot, J., McCready, P.M., Kobayashi, A., Ow, D., Carrano, A.V. and Garcia, E.
Direct Submission

Birect Submission

Birect Submission

Birect Submission

Birect Submission

CA 94550, USA

Genomic Structure of the Human MEP2B Gene
Genomic Structure assembled from coverlapping cosmids R30102 (bases 1-36,229), R29350 (bases 29,365-71,464), and R27740 (bases 54,941-89,818).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LL19NCO3 library constructed at LLNL from flow-sorted chromosomes from hybrid 5H12-B, which carries chromosome 19 as its only human chromosome" complement(177 + 452) /rpt_family="ALU" /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /orce="hypothetical partial orf most similar to orf from C. elegans cosmid F43G9.3 (279755): putative exon, Xgrail 1.3c, excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens DNA from chromosome 19-cosmids R30102:R29350:R27740 containing MEF2B, genomic sequence, complete sequence.
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/cell_line="5HL2-B"
/cell_type="fibroblast"
/clone_lib="LL19NC03 R chromosome 19-specific cosmid
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89818)
Lamerdin,J.E.
                     /note="AluJb repeat: matches 293. .1 of consensus" 46958. .47286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 1; Pred. No. 5.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p12"
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1. .89818
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/product="R31240_1"
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Anote-"AluSx repeat: matches 293. .5 of consensus"

30498 .30588

Anote-"MIR2 repeat: matches 1. .96 of consensus"

31144 .31698

Anote-"LiME1 repeat: matches 545 .1088 of consensus"

3748 .34075

Anote-"LiME1 repeat: matches 533 .290 of consensus"

34358 .34655

Anote-"AluJo repeat: matches 301 .1 of consensus"

35506 .35516

Anote-"MES or peat: matches 230 .1 of consensus"

35953 .36259
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Anotes Aludos repeat: matches 301. .9 of consensus" 39850. .39964

Anotes MIR2 repeat: matches 5. .125 of consensus" 40247. .40290

Anotes ILMB3 repeat: matches 923. .880 of consensus" 40291. .40470

Anotes TAM repeat: matches 174. .5 of consensus" 40475. .40598

Anotes ILMB2 repeat: matches 880. .757 of consensus" 40475. .40784

Anotes ILMB8 repeat: matches 176. .314 of consensus" 40597. .40744
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                            prim_transcript 16256. 17096
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1762. .41907
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1694. .41761
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note="MSTD re
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/note="BLASIN similarity to H03990 (387426); match: 0.9, score: 3.4e-142; database searched: est; yj47b08.s1 Homo sapiens cDNA clone 151863 3'." complement(32433284) /note="BLASIN similarity to H03990 (347388); match: 0.95, score: 3.4e-142; database searched: est; yj47b08.s1 Homo sapiens cDNA clone 151863 3'." complement(32553284) /note="BLASIN similarity to R10902 (336365); match: 0.76, score: 2.1e-117; database searched: est; yf58f01.s1	Homo sapiens cDNA clone 129145 5'." complement(32663249) to R22559 (356374); match: /note="BLASTN similarity to R22559 (356374); match: 0.94, score: 1.1e-108; database searched: est; yh23h12.s1 Homo sapiens cDNA clone 130631 3'. >qb G30262 G30262 human STS SHGC-3640"	complement(32703318) /note="BLASIN similarity to R10902 (301349); match: 0.85, score: 2.8e-125; database searched: est; yf38f01.s1 Homo sapiens cDNA clone 129145 3'." complement(32813318) /note="BLASIN similarity to H03990 (312349); match: 0.73, score: 3.1e-97; database searched: est; yj47b08.s1 Homo sapiens cDNA clone 151863 3'."	complement(32973432) /note="BLASTN similarity to H03990 (197332); match: 0.97, score: 3.4e-142; database searched: est; y347b08.s1 Homo sapiens cDNA clone 151863 3'." complement(32973321) /note="BLASTN similarity to R48002 (306330); match: 0.92, score: 1.1e-95; database searched: est; y363905.s1	Homo sapiens cDNA clone 153464 3'." complement(32983621) /note="BLASTN similarity to 239994 (1324); match: 0.99, score: 6.2e-126; database searched: est; H. sapiens partial cDNA sequence"	complement(33103362) /note="BLASTN similarity to R22559 (272324); match: 0.83, score: 1.1e-108; database searched: est; yh23h12.s1 Homo sapiens cDNA clone 130631 3'. >gb[G30262 G30262 human STS SHGC-36640"	33103339 /note="BLASTN similarity to R48116 (353382); match: 0.8, score: 2.0e-134; database searched: est; yj63g05.r1 Homo sapiens CDNA clone 153464 5'." complement(33103432) /note="BLASTN similarity to R10902 (186308); match:	0.97, SCOTE: 1.08-125; database searched: eSt; yistolisi Homo sapiens CDNA clone 129145 3'." Complement(3322. 3362) /note="BLASTN similarity to R48002 (262. 302); match: 0.97, score: 1.1e-95; database searched: est; yj63905.s1 Homo sapiens CDNA clone 153464 3'."	3332. 3397 /note="BlASTN similarity to R48116 (379444); match: /note="BlASTN similarity to R48116 (379444); match: 0.74, score: 2.0e-134; database searched: est; yj63g05.rl Homo sapiens cDNA clone 153464 5." complement(33363432) /note="BLASTN similarity to H68521 (192288); match:	<pre>0.97, SCORE 1.99-106; database searched: est; yublbul.sl Homo sapiens cDNA clone 229611 3'." Complement(3339 . 3391) /note="BLASTN similarity to R22559 (242294); match: 0.66 . score: 5.6e-102; database searched; est; yh23h12.sl Homo sapiens cDNA clone 130631 3'. >qb G30262 G30262 human</pre>	STS SHGC.36640" complement(33713624) /note="BLASTN similarity to Z16003 (1254); match: 0.95, score: 3.5e-89; database searched: est; H. sapiens partial cDNA sequence, clone 56B12" complement(33753629) /note="BLASTN similarity to R22559 (2256); match: 0.98, score: 1.1e-108; database searched: est; yh23h12.s1 Homo
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  sapiens cDNA clone 130631 3'. >qb|G30262|G30262 human STS SHGC-36640"
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CDNA clone 130631 3'. >9b|G30262|G30262 human STS
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                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 93841)
                                                                                                                                                                                                                                                                                                                                                                                                                       www.jgi.doe.gov.
**Working draft' sequence. It currently
**Consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* trus of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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PROGRESS ***, 60 unordered pieces.
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Sequencing of Human Chromosome 5
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Submitted (06-0CT-1999) Production Sequencing Facility, DOE Joint Submitted (06-0CT-1999) Production Sequencing Facility, DOE Joint Secone Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, 0SA * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                              AC011336 96099 bp DNA HTG 06-0CT-1999
Homo sapiens chromosome 5 clone CIT-HSPC_250113, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.
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                                                 Score 18; DB 32; Length 95425; Pred. No. 5.8;
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1367: contig of 662 bp in length
1367: contig of 662 bp in length
2143: contig of 776 bp in length
2940: contig of 776 bp in length
38p of unknown length
38p of unknown length
38p of unknown length
4813: contig of 1873 bp in length
7980: contig of 1873 bp in length
7980: contig of 1875 bp in length
49500: contig of 41520 bp in length
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24003 c 24571 g 24303 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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DOE Joint Genome Institute.
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Matches 18; Conserv
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Homo sapiens chromosome X clone J506G21, *** SEQUENCING IN PROGRESS
***, in unordered pieces.
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Cambridgeshire, CB10 1SA, UK. E-mail enquires:
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
Confer of segments is not known; 800 n's separate segments.
Unfinished sequence: dJ50662 Contig_ID: 01828 Length: 797 bp Unfinished sequence: dJ50662 Contig_ID: 01927 Length: 77027 bp Unfinished sequence: dJ50662 Contig_ID: 01957 Length: 1258 bp Unfinished sequence: dJ50662 Contig_ID: 00779 Length: 1258 bp Unfinished sequence: dJ50662 Contig_ID: 00779 Length: 53943 bp.
* NOTE: This is a "working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
I (bases 1 to 95425)
Unknown.
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52956: contig of 1953 bp in length gap of unknown length contig of 1188 bp in length gap of unknown length contig of 167 bp in length gap of unknown length
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gap of unknown length
93841: contig of 25509 bp in length.
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23592 c 24325 g 23115 t
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/db_xref="taxon:9606"
/chromosome="x" /clone="J506G21"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                     AC013370 100091 bp DNA HTG 20-NOV-1999
Homo sapiens clone RP11-12D16, LOW-PASS SEQUENCE SAMPLING.
AC013370
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 100091) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-12D16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 110 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-fich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.
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                               RESULT 38
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AUTHORS
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JOURNAL
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COMMENT

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Direct Submission

Direct Submission

Bundated (16-MAR-1998) sanger.ac.uk/HGP/Chrl/) Sanger Centre,
Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires:
Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires:
Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires:

Numqueryesanger.ac.uk Clone requests: clonecrequest(sanger.ac.uk

On Mar 28, 1998 this sequence version replaced gi:257807.

IMPORTANT: This sequence is not the entire insert of clone 262012.
It may be shorter because we only sequence overlapping sections
once, or longer because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.

265012 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/ The true
left end of clone 262012 is at 100895 in this sequence. The true right
end of clone 262012 is at 1 in this sequence.

1 contract the repeats of the resolve all in the repeated of the resolve the
                                                                                                     Cytotactin; Hexabrachion; mitochondrial 30S ribosomal; Myotendinous antigen; Neuronectin; S14; Tenascin.
 Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30s ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_"RP1-262D12"
/clone_lib="RPCI-1"
708. _1270
/note="MER25 repeat: matches 1556. _2130 of consensus"
                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100997)
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Note="AluSq repeat: matches 133. 1 of consensus; incompleter repeat"
3948. 4733

/note="L1 repeat: matches 4617. 5390 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2184 of consensus"
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/note="AluSx repeat: matches 302.
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/note="L1 repeat: matches 2239.
2498. 3316
/note="L1 repeat: matches 3786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1723. .1915

//note="L1 repeat: matches 1993.

1919. .2224

/note=AluSx repeat: matches 1.

2308. .2495
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="q23.3-24.3"
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                                                                                       299297.1 GI:2995179
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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if unknown length
g of 937 bp in length
of unknown length
                                                                                                                                                                                                                                                                                    f unknown length
g of 928 bp in length
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937 bp in length
                unknown length
of 951 bp in length
                                                  unknown length
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of 934 bp in length
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of 931 bp in length
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of 906 bp in length
unknown length
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of 920 bp in length
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of 953 bp in length
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   in length
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known length
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of 939 bp in length
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of 955 bp in length
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unknown length
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of 913 bp in length
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Best Local Similarity 100.
Matches 18; Conservative
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HS262D12
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A9900. 35524

A00te="MERSA repeat: matches 1. .133 of consensus"
36555. 36674

Anote="MIR repeat: matches 161. .28 of consensus"
36552. 36934

Anote="MIR repeat: matches 100. .142 of consensus"
37851. 38094

Anote="MIR repeat: matches 100. .142 of consensus"
37851. 38094

Anote="MIR repeat: matches 118. .29 of consensus"
37850. .39989

Anote="MIR repeat: matches 118. .29 of consensus"
Anote="MIR repeat: matches 249. .2 of consensus"
Anote="MIR repeat: matches 302. .1 of consensus"
Anote="MIR repeat: matches 302. .1 of consensus"
Anote="MIR repeat: matches 303. .1 of consensus"
A1912. A1912
Anote="MIR repeat: matches 303. .1 of consensus"
A1912. A6215
Anote="MIR repeat: matches 303. .1 of consensus"
A1912. A6215
Anote="MIR repeat: matches 303. .1 of consensus"
A1912. A6215
Anote="MIR repeat: matches 303. .1 of consensus"
A1912. A6215
Anote="MIR repeat: matches 303. .2 of consensus"
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Anote="Alusq repeat: matches 303. .2 of consensus"
Anote="Alusq repeat: matches 303. .2 of consensus"
Anote="Alusq repeat: matches 125. .301 of consensus;
Anote="Alusq repeat: matches 125. .301 of conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        incomplete repeat"
53563. 53606
Anotes 24 copies of 2 mer 100 % conserved"
54397. 54556
Anotes LIME2 repeat: matches 735. .902 of consensus 54654. 54844
54654. 54844
55009. 55150
'note="AluJb repeat: matches 302. .129 of consensus;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                        33402. .33473
/note="MIR2 repeat: matches 75. .146 of consensus"
34856. .34881
/note="13 copies of 2 mer 96 % conserved"
34900. .35024
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AL049761.10 GI:5738437
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HSDJ863C7/c
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SOURCE
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29346. .29435,30905. .31090,34414. .34677,35133. .35507,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="dJ262D12.1 (Tenascin (Hexabrachion, Cytotactin,
Meronectin, Myotendinous antigen) LIKE protein;
/protein_id="CB1600.1"
/db_xref="G1:2995180"
/db_xref="G1:2995180"
/db_xref="SPTREMBL:060782"
/tb_xref="SPTREMBL:060782"
/tb_xref="SPTREMBL:060782"
/tb_xref="SPTREMBL:060782"
/tb_xref="NREQQVIVSHTYKIDVPKSALVQVDADPQPLSDDGASLLALGEA
REEDANIFRHNIRLOTPGADCEAGSVQDLLARVKKLEEEMYEMKEGCSAQRCCQGVT
DLSRHCSGHGTFSLETCSCHCEEGREGAACERLACPGASGHGRCVDGRCLCHEPTVG
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KRQHSYELIGLLPGTKYIVYLBNVKNENSSSPQHLLATYDLAVUGTAWTDETENSLD
VEWBRPSTEVDY KLENGPMTGQEVAENTYPOSPRSLD
KRELEGK PILLNGRTEIDSPTNVVTDRVTEDTATVSMDPVQAVIDKYVVRTSADGDT
KRANTHNEDSSSTVLTGLRFGEXYKVYNAERGNGSKRADTNALTEIDSPANLYDRV
TENATISWPDVQATIDKYVNRYTSADQETREVLOGREGSSTVLTGLREPGYBTYTHY
WAQKGDRESKKADTNAPIDIDSPKNLYTENDRYTENMATVSWDPVQAAIDKYVVRYTSAG
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090826 090994 P10039 005546 000546 000210; match: mRNAs
M23121 J04519 X56304 D90343 X61599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Limada repeat: matches 835. .1046 of consensus" 14502. .14669 /note="MER00 repeat: matches 33. .216 of consensus" 15152. .15450 /note="13 copies of 23 mer 84 % conserved"
                                                                                                                                                                                                                         7384. 7832
/note="pTR5 repeat: matches 69. .489 of consensus"
9120. 11729
/note="match: mRNAs M85205 X57147; match: genomic DNA
294650; matches many viral proteins; remnants of
endogenous retrovirus"
                                                                                      /note="pTR5" repeat: matches 504. .2438 of consensus"
13764. .13978
                                                                                                                                                                      8814. .7590
'note="pTR5 repeat: matches 739. .2429 of consensus"
                                                     1453. :5760
| note="Alurb8 repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 98. .207 of consensus" 26440. .27235
/note="MER21B repeat: matches 790. .2 of consensus" 27314. .27744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 129. .15 of consensus" 21349. .21467
/note="MIR2 repeat: matches 145. .27 of consensus" 21522 . .21252
/note="MIR2 repeat: matches 2. .302 of consensus" 23253. .23280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consensus
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consensus matches 303. .4 of consensus" 29829. 30002
                                'note="L1MA5 repeat: matches 1. .800 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSq repeat: matches 1, .303 of consensus" 9749. .19859
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17987. .18146
/note="MIR repeat: matches 49. .215 of consensus"
18956. .19268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MER4C repeat: matches 24. .472 of .27968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(16245. .37320)
/gene="dJ262D12.1"
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Gaps

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Db 78298 CCACCGCACCTGGCTGAT 78315
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Matches 18; Conservative
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AC015845_0
AC015845_1
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AC015845_3
AC015845_4
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AC010679_0
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AC010679_2
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AC015845_0/c
WPCOMMENT
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AC010679_2
WPCOMMENT
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                                                              Direct Submission

Direct Submission

CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requestes: clonerequest@sanger.ac.uk

On Aug 18, 1999 this sequence version replaced gi:5708178.

On Aug 18, 1999 this sequence version replaced gi:5708178.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at the entire inser ac.uk/Projects/C_elegans/wormpep This sequence is the entire inser ac.uk/Projects/C_elegans/wormpep This sequence is the entire inser of clone 86377. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' faature key.

This sequence as generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 human chromosome 20, constructed by the Sanger centre Chromosome 20 human chromosome 20, constructed by the Sanger Centre Chromosome 20 human chromosome 20. constructed by the Sanger Centre Chromosome 20 human chromosome 20 constructed by the Sanger centre Chromosome 20 constructed by the Sanger Centre Chromosome 20 constructed by the Group of Pieter de Jong. For further contains field.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS112K5 109891 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 112K5 on chromosome Xpl1, complete
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Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 109891)
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23899 c 22881 g 30298 t
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/db_xref="taxon:9606"
/chromosome="20"
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/clone_lib="RPCI-5"
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1 (bases 1 to 109210)
Blakey, S.
Direct Submission
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Z85987.13 GI:5531490
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Best Local Similarity 100.
Matches 18; Conservative
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DEFINITION
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HS112K5/c
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AC010679_3 300001 350997
Continuation (3 of 4) of AC010679 from base 200001 (AC010679 Homo sapiens clone NH012
together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL
This sequence is the entire insert of clone 112K5. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
112K5 is from the library RPCII constructed at the Roswell Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
Location/Qualifiers
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/clone_lib="RPCI-1"
25957 c 26406 g 28171
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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gap of unknown length contig of 787 bp in length gap of unknown length contig of 801 bp in length
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unknown length
of 751 bp in length
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of 780 bp in length
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of 791 bp in length
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of 784 bp in length
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E. Chases 1 to 573550)
E. Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Cooke, P., DeArellano, K., Dewar, K., Gage, D., Galagan, J., Gardyna, S., Grant, G., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Mann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKenan, K., McLamghlin, J., Meldrim, J., McTorow, J., Naylao, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Leboats, Were identified using RepeatMasker:
Smit, AF. A., & Green, P. (1996-1997)
LILLIN, AF. P. R. Green, P. (1996-1997)
LILLIN, AF. P. & Green, P. (1996-1997)
                                                                                                                                                              Eucharia, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 573550)
                       17-NOV-1999
AC015845_5 500001 573550

AC015845 573550 bp DNA
NITION HOMO Sapiens chromosome 17 clone RP11-343K8 map 17, LOW-PASS
SEQUENCE SAMPLING.
SSION AC015845.1 GI:6446823
CON AC015845.1 GI:6446823
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
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COMMENT

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L Submitted (13-8.00)

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: Smit, A.F.A. &

Green, P. (1996-1997)

Http://ftp.genome.washington.edu/RM/RepeatMasker.html.

* NOTE: This record contains 153 individual

* Sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 121345)

Birrar, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone 20_1_21
                                                                                                                                                                                                             HTG 13-NOV-1999
LOW-PASS SEQUENCE SAMPLING.
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186: contig of 785 bp in length
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; contig of 81'.
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Homo sapiens clone 20_1_21,
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                                                      29319 CCACCGCACCTGGCTGAT 29302
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HTG; HTGS_PHASE0.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		T98890 ve65f09.rl	H18435 ym43b05.s1
		ID		T98890	493 23 H18435
		DB	1	21	23
		Length		405	493
æ	Query	Match		72.5	50.4
		No. Score Match Length DB ID	1 1 1 1 1 1	198.6	2 138 50.4
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	Resu	4			O

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Email: est@watson.wustl.edu
Insert Size: 1065
High qality sequence stops: 279 Source: IMAGE Consortium, LLNL This
High qality sequence stops: 279 Source: IMAGE Consortium, LLNL This
Consortium (info@image.llnl.gov) for further information.
Insert Length: 1065 Std Error: 0.00
Seq primer: MI3RP1
High quality sequence stop: 279.
High quality sequence stop: 279.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 493)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GAACTACAAAGGGATCGGTGCCTATATCACAATACCAAACTTGATAATAATCTAGATTCT 90
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ym43b05.s1 Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:50988 3', mRNA sequence.
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The WashU-Merck EST Project
Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:811454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.5%; Score 198.6; DB 21; Length 405; Best Local Similarity 98.7%; Pred. No. 2.1e-36; Matches 220; Conservative 1; Mismatches 0; Indels 2;
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H18435.1 GI:884675
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A1534828 MA000097.
A1532181 KSB504.x
A0570963 HS_535_B
AA755877 vv36604.r
AA550066 1160m3 gm
AA550066 1160m3 gm
AA550264 HS_3040_B
A0129266 HS_3040_B
A1106619 Drosophil
AL052544 Drosophil
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AQ139258 HS_3090_A
AQ326393 nbxb0031J
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AA17894 WV05eQ2.r
AA873942 vw86a03.r
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H09173 y198h02.sl
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291988 F. rubripes
ALIOGO08 Drosophil
R45421 y942f02.s1
ALIO6396 Drosophil
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AQ587717 CITBI-E1
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AI860086 tx73d01.x
AI811918 tw76c09.x
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1965f09.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone
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AL107647 Drosophil
AL104817 Drosophil
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AV373585 AV373585
AI395037 MA002262.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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The Wash-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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FR0008178
CNS015WU
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AQ620120
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AQ570963
AA755877
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AQ836402
AQ836402
AO129266
CNSO116DT
CNSO118G8
CNSO1176D
CNSO1176D
ANTRONSO176D
ANTRONS
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CNS010L9
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AA488906
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AV373585
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LOCUS DEFINITION

RESULT 198890

ACCESSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Homo sapiens
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es 128; Conserv
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Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1071
High quality sequence stops: 327
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: This clone is available royalty-free through LLNL: INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1071
Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 327.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                     /db_xref="taxon:9506"
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Pred. No. 1.7e-22;
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F03205
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77.38;
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Matches 218; Conservative
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Corenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 CIGAAACAGCCTAACAITITACAAAATITITAGTITITCTITITIAGAGICTIATACCTGTAG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 CTATATAACAGTTCATGTCTGATTTAGCATTTGTTCACGAGTAAAGCTGGAACTATGAAA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genexpress@genethon.fr
Single read. removed at sequence 5'end
Genexpress_lbrary_idt: C; Genexpress_sequence_idt: alc-lpf07
Seq primer: (-21)M13_universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="c-lpf07"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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.larity 99.2%; Pred. No. 5.2e-20;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                       and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1,rue de l'Intern
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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us-09-090-672b-12.rst

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Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Unpublished (1996)
Unsuplished (1996)
Unsuplished (1996)
Unsuplished (1996)
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 459)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vw86a03.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone impGE:1261804 5' similar to TR:O14432 O14432 TUP1.;' mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGTTTACAGATTCTCTTGCGGCTGGCGGTGGAACTACAAAGGGATCGGTGCCTATATCAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.2%; Score 113; DB 30;
94.3%; Pred. No. 1.1e-16;
iive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                 Seg primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 297. Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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Best Local Similarity
Matches 116; Conserv
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Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152443.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-11550
Email: Robert_Strausberg@ih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLOR distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 318)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsells.T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA197894 318 bp mRNA EST 12-MAR-1997 mv05e02.rI GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA clone_IMAGE:654170 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 AATACCAAACTIGATAATAATACTAGATTCTGTGTGTCTCTGCTTATAGACCATGTTTGTAGT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1493205"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%; Score 117.8; DB 39; llarity 96.7%; Pred. No. 8.1e-18; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 1846 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 365.
Location/Qualifiers
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Matches 119;
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AA197894
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Length 318; Indels USA

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ligated to a Drail adaptor [CTTTGGCCTACTGG], digested and cloned into distinct Drail sites of the pME18s-FL3 wector (5' site CACTGTGG, 3' site CACCATGGG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTRAAAGGTGGG and 3' end primer CGACCTGCAGGACA."
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1 (bases 1 to 31)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pME188-FL3; Site_1: DraIII
(GACTGTGT); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA432984 391 bp mRNA EST 04-AUG-1997 ve87bl2.sl Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:833183 5', mRNA sequence.
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On Mar 10, 1998 this sequence version replaced gi:2948074. Contact: Marra M/Washbr.NCI mouse EST project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, US Fax: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111.4; DB 74; Length 731;
Pred. No. 2.2e-16;
1; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2099297"
/clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"/strain="C57BL"
                                                                                                                                                                                                                                                                                                              Seg primer: custom primer used
High quality sequence stop: 521.
Location/qualifiers
1..731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
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Best Local Similarity 93.5%;
Matches 115; Conservative
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Mus musculus
                                                                                                                                                                                                                                                                                    MGI:996229
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ORIGIN
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AA432984
LOCUS
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Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 731)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
The WashU-NOT Mouse EST Project 1999
Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811146.
Contact: Maran M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HMI Mouse EST Project
WashD-HMI Mouse EST Project
Fat: 144 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 514 286 180
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ul24h09.yl Sugano mouse kidney mkia Mus musculus CDNA clone
IMAGE:2099297 5' similar to TR:031259 031259 VANADIUM
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/db_xref="taxon:10090"
/clone="IMAGE:1261804"
/clone_lib="Stratagene mouse skin (#937313)"
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                                                                                                                                                                                                                                                                                                                                                                                      primer: -28ml3 rev1 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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Location/Qualifiers
1. .459
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Best Local Similarity
Matches 116; Conserv
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| AGG 163
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         JOURNAL
COMMENT
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                      WashU-HHM Mouse EST Project
WashU-HHM Mouse EST Project
WashU-HHM Mouse EST Project
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
1441 Ed. 1800
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Famil: mouseset@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:49339
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers
I. companism="Mus musculus"
/Abrain="B6D2 F1/J"
/Ab_xref="taxon:10090"
/clone="ImAGE:83183"
/clone="ImAGE:83183"
/fissue_trype="embryo"
/db_bost="DH108"
//lb_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: embryo; Vector: pBluescribe (modified); Site_1: Mlu1; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: Sal1(dT): 5-CGGTCGACCGTCGACGTTTTTTTTTTTTTTTTTTT.3', cDNAs were cloned into the Mlu1/Sal1 sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 387).

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AACTIGATAATAATCTAGATTCTGTGTYTCTGCTTATAGACCATGTTTGTAGTAGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AACTGGACAAGAATCTAGATTCTGTGTCTCTACTTATAGATCATGTTTGTAGTAGG 217
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:804216.
Contact: Marra M/Mouse EST Project
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Pred. No. 4.7e-11;
1; Mismatches 17;
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83 c 96 g
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H09173
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Best Local Similarity 84.5%;
Matches 98; Conservative
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I (Dases 1 to 274)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhand, M.M., Fritchman, J.E., Googhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.G., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., Moboand, L.A., Nouyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
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                                                                                            Insert Size: 1081
High quality sequence stops: 314
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1081 Std Error: 0.00
Seq primer: Promega -21ml3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 ITACAAAATTTTAGTTTTCTTTTTAGAGT -- CTTATCCTGTAG - CTATATAACAGTTCA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 CCATGTTTGTAGTAGGTA-AGAGGAAAACTTCC---TATATTCTGAAACAGCCTAACATT 163
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MO 63108
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  Louis,
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Pred. No. 1.5e-09;
Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
29.9%; Score 81.8; D
Best Local Similarity 85.7%; Pred. No. 1.5e
Matches 150; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                           High quality sequence stop: 314.
Location/Qualifiers
                                                                                   Email: est@watson.wustl.edu
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10.353
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Columbia University
Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
10032
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 ACAATACCAAACTTGATAATAATGTTGGATTCTGTGTYTCTGCTTATAGACCATGTTTGTA 118
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                                                                                                                                                                                                                                                                                               Construction and characterization of a normalized Proc. Natl. Acad. Sci. U.S.A. 91, 9228-9232 (1994) 95023884
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                                                                                        Bonaldo, Ph.D. cDN Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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Pred. No. 1.3e-05;
1; Mismatches 0;
                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
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Best Local Similarity 98.5%;
Matches 64; Conservative 1
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Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Dednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D.P., Feng,D.F., Ferie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.W., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (5547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699035
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 IGCCIATATCACAATACCAAACTTGATAATAATCTAGATTCTGTGTTYTCTGCTTATAGAC 108
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 559)
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397871.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                        On Dec 3, 1996 this sequence version replaced gi:1119186.
Other_ESTs: THC126123
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 7.4e-08;
1; Mismatches 0; Indels 0
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The Institute for Genomic Research
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Best Local Similarity 98.7%;
Matches 74; Conservative
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//dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost="dex_bost=
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1 (Dases 1 to 449)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Laroy,M., Le,M., Martin,J., Morits,M., Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B., Theising,B., Mylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is avallable royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:970632
                                                                                                                                                                                                                                                                                             1 CGTTTACAGATTCTCTTGCGGCTGGCGGTGGAACTACAAAGGGATCGGTGCCTATATCAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI196903 449 bp mRNA EST 14-OCT-19
ui55c03.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1886308 5' similar to TR:014432 014432 TUPI. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashJ-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
WashJogton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                               Length 596;
                                                                                                                                                                                           4; Indels
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/db_xref="taxon:10090"
/clone="INAGE:1886308"
/clone_lib="Sugano mouse liver mlia"
                                                                                                                            Query Match 23.2%; Score 63.6; DB 104; Best Local Similarity 94.3%; Pred. No. 2.2e-05; Matches 66; Conservative 0; Mismatches 4;
             ų
          203
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High quality sequence stop: 448.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 596)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ,
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
thrp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calfech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 CTTATCCTGTAGCTATATAACAGTTCATGTCTGATTTAGCATTTGTT-CACGAGTAAAGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ587717 596 bp DNA GSS 07-JUN-1999 CITBLE: E1-2646F4.TF CITBL E1 Homo sapiens genomic clone 2646F4, genomic survey sequence.
AQS87717 GI:5014397 AQ587717.1 GI:5014397
                                                                                                                                                                                                                                                                                                                                     /lab_host="E. coll"
//lab_host="Vector: Lafmid BA: Site_1: Not I; Site_2: Hind
Size-selected cDNA from polyA+ RNA from human brain.
3-month old meonate.This library is the result of an attempted normalization of library b4HB3MA."
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Pred. No. 1.8e-05;
0; Mismatches 4; Indels 1
                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="b4HB3MA-COTB-HARP-Ft.387"
/clone_lib="b4HB3MA Cot8-HARP-Ft"
Tel: 2129602313
Fax: 2127813577
Email: cuc@cuccfa.ccc.columbia.edu
antisense, Ampicillin
Seq primer: M13 Forward (Universal).
Location/Qualifiers
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7. crganism="Homo sapiens"
7. db_xref="taxon:9606"
7.clone="7.84,674"
7.clone="1.16-"CITBI-EI"
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Best Local Similarity 93.94
Matches 77; Conservative
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AQ587717
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Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
V_type: phage
PRIMER: M13
                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
                                                                                                                                                                                                                                                                                                    FR0008178 614 bp DNA GSS 02-MAR-1997 C. Lubripes GSS sequence, clone 188G03aD4, genomic survey sequence. 291988 1 GI:1869202
                                                                                                                        61 AATACCAAACTTGATAATAATCTAGATTCTGTGTYTCTGCTTATAGACCATGTTTGTAGT 120
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Best Local Similarity 61.2%; Score 53.8; DB 79; Length 614;
Best Local Similarity 61.2%; Pred. No. 0.004;
Matches 85; Conservative 1; Mismatches 53; Indels 0
                                                              Length 449;
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                                                                                            Indels
                                                            Score 62.8; DB 43;
Pred. No. 3.5e-05;
1; Mismatches 3;
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/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone="lib="cosmid 188G03"
/clone="lib8G03a04"
a 159 c 159 g 145 t
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                                                            Query Match
Best Local Similarity 94.1%;
Matches 64; Conservative
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 82
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Search completed: April 5, 2000, 11:35:51 Job time: 22828 sec

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